

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 14, 2005, 15:03:35 ; Search time 43 Seconds
(without alignments)
1458.915 Million cell updates/sec

Title: US-10-614-076-98

Perfect score: 3406

Sequence: 1 MNPNNRSEHDTIKVTPNSEL.....SFVSNKIVYDKIEFIPVQL 652

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	100.0	652	2	I39811
2	3212	94.3	659	2	I10228
3	2341.5	68.7	652	2	A27223
4	2152	63.2	649	1	JH0261
5	1127.5	33.1	1157	1	S49247
6	1124.5	33.0	719	2	I40590
7	1119	32.9	1138	2	A48944
8	1100.5	32.3	719	2	I39815
9	1091.5	32.0	719	2	I39814
10	1091.5	32.0	719	2	S25383
11	1072.5	31.5	1228	2	S00873
12	1060	31.1	1160	2	I40589
13	963.5	28.3	1154	2	S39536
14	934.5	27.4	655	2	JC7140
15	926.5	27.2	1189	2	S00944
16	907.5	26.6	823	2	S04181
17	906.5	26.6	1155	2	S02134
18	900.5	26.4	1155	2	A26513
19	899.5	26.4	1155	2	JD0002
20	899.5	26.4	1156	2	A24125
21	898.5	26.4	1174	2	A42459
22	895.5	26.3	1155	2	I39838
23	888	26.1	1181	2	A41052
24	886.5	26.0	1176	2	A48970
25	876	25.7	1176	2	JT0241
26	874	25.7	934	2	A22798
27	870	25.5	1176	2	JC2219
28	869.5	25.5	1171	2	I40572
29	869.5	25.5	1171	2	A37829

30	867.5	25.5	1177	2	A49785	parasporal crystal
31	867	25.5	1178	1	USBSKH	parasporal crystal
32	866.5	25.4	1166	2	S32645	parasporal crystal
33	866	25.4	1176	2	A22617	parasporal crystal
34	866	25.4	1176	2	S02215	parasporal crystal
35	861.5	25.3	618	2	S11445	parasporal crystal
36	845	24.8	1174	2	S32649	parasporal crystal
37	838.5	24.6	1165	2	S11446	parasporal crystal
38	828	24.3	1160	2	S32647	parasporal crystal
39	809	23.8	1156	2	A29838	parasporal crystal
40	787.5	23.1	1172	2	S32689	parasporal crystal
41	700	20.6	380	2	B42459	hypothetical prote
42	679	19.9	1156	2	S19306	parasporal crystal
43	665.5	19.5	934	2	B29838	parasporal crystal
44	656.5	19.3	1136	1	USBS81	parasporal crystal
45	637.5	18.7	1180	2	I39870	parasporal crystal
46	634.5	18.6	1180	2	A26858	parasporal crystal
47	482	14.2	613	2	JC6033	mosquitocidal prot
48	279.5	8.2	1245	2	T18211	delta endotoxin -
49	245.5	7.2	633	2	C32053	parasporal crystal
50	245	7.2	633	2	D32053	parasporal crystal
51	236	6.9	1385	2	T18213	parasporal crystal
52	233	6.8	282	2	A25140	parasporal crystal
53	228.5	6.7	1289	2	T18212	parasporal crystal
54	228	6.7	622	2	S17402	parasporal crystal
55	219.5	6.4	643	2	A43647	parasporal crystal
56	215.5	6.3	1186	2	T18210	delta endotoxin -
57	138	4.1	904	2	G90563	lipoprotein limpor
58	129.5	3.8	2139	2	S46404	vitellogenin - yel
59	127.5	3.7	1513	2	S45768	mitotic spindle pr
60	126	3.7	937	2	G97168	glycosyltransferas
61	125.5	3.7	1193	2	S68218	botulinum neurotox
62	124	3.6	753	2	AG1710	maltosephosphoryla
63	121.5	3.6	1138	2	A82939	membrane nuclease
64	121.5	3.6	2529	2	B64635	toxin-like outer m
65	120.5	3.5	1193	2	JC4901	non-toxic-nonhemagg
66	120	3.5	545	2	F86834	alpha-glucosidase
67	119.5	3.5	835	2	E72305	hypothetical prote
68	119.5	3.5	1946	2	JC6032	lactocepin (EC 3.4
69	119	3.5	773	2	JEO387	exo-alpha-sialidas
70	119	3.5	1474	2	T18281	hypothetical prote
71	118	3.5	1127	2	T28317	ORF MSV156 hypothe
72	118	3.5	1285	2	S70582	botulinum neurotox
73	118	3.5	2166	2	G70163	hypothetical prote
74	117.5	3.4	753	2	A11339	maltosephosphoryla
75	117.5	3.4	2399	2	H71879	toxin-like outer m
76	117.5	3.4	4888	2	F82885	hypothetical prote
77	117	3.4	1175	2	F64489	hypothetical prote
78	117	3.4	2334	2	S32920	cell wall-associat
79	116.5	3.4	767	2	F71479	hypothetical prote
80	116	3.4	804	2	A53211	glucose-regulated
81	115.5	3.4	1276	2	S11455	botulinum neurotox
82	115	3.4	770	2	A11769	autolysin, amidase
83	115	3.4	802	2	A29317	endoplasmic reticu
84	114.5	3.4	376	2	A90206	histidinol-phospha
85	114.5	3.4	863	2	G96964	probable permease,
86	114.5	3.4	1193	2	G71605	hypothetical prote
87	114.5	3.4	1516	2	E71619	RAD2 endonuclease
88	114	3.3	713	1	ALBSG1	cyclomaltodextrin
89	114	3.3	803	2	A35954	endoplasmic precu
90	114	3.3	925	2	D59105	hypothetical prote
91	114	3.3	1118	2	T28426	probable DNA-direc
92	114	3.3	1407	2	S59823	probable membrane
93	114	3.3	2244	2	F90563	hypothetical prote
94	113.5	3.3	547	2	G69620	ATP-binding transp
95	113.5	3.3	1806	2	AF1717	probable peptidogl
96	113	3.3	644	2	T21137	hypothetical prote
97	113	3.3	749	2	T31536	hypothetical prote
98	113	3.3	1209	2	AH2052	hypothetical prote
99	113	3.3	1477	2	T18534	protein-tyrosine k
100	112.5	3.3	566	2	TS0382	probable spindle p
101	112.5	3.3	2401	2	T28676	thorpy protein -
102	112	3.3	1375	2	S48375	hypothetical prote

103 111 3.3 1017 2 T18488
104 111 3.3 1067 2 T28663
105 111 3.3 1658 2 S55101
106 111 3.3 2910 2 T28156
107 110.5 3.2 520 2 T18124
108 110.5 3.2 2485 1 H71621
109 110 3.2 725 2 T19994
110 110 3.2 814 1 C40618
111 110 3.2 1616 2 T16600
112 109.5 3.2 957 2 H97800
113 109.5 3.2 986 2 E90596
114 109.5 3.2 1103 2 H82884
115 109.5 3.2 1119 2 B70126
116 109 3.2 726 2 S62180
117 109 3.2 804 2 S51358
118 109 3.2 1202 1 S05362
119 109 3.2 2819 2 A90551
120 108.5 3.2 640 2 T03754
121 108.5 3.2 775 1 VPRW6
122 108.5 3.2 4450 2 JX0340
123 108.5 3.2 4550 2 T18440
124 108 3.2 593 2 F64523
125 108 3.2 851 2 S06670
126 108 3.2 986 2 H90565
127 107.5 3.2 1086 2 T43266
128 107.5 3.2 1086 2 T43266
129 107.5 3.2 1468 1 S30818
130 107.5 3.2 1790 1 S27772
131 107 3.1 300 2 T08453
132 107 3.1 1048 2 H64459
133 107 3.1 1599 2 S22737
134 107 3.1 2178 2 S58805
135 107 3.1 2364 2 I40884
136 107 3.1 3262 2 AH2137
137 107 3.1 4196 2 T43274
138 106.5 3.1 822 2 AB2507
139 106.5 3.1 834 2 B82940
140 106.5 3.1 891 2 G89957
141 106.5 3.1 945 2 A64714
142 106.5 3.1 1272 2 S60999
143 106.5 3.1 1279 2 E64709
144 106.5 3.1 1959 2 AG1085
145 106.5 3.1 4563 1 LPHUB
146 106 3.1 485 2 E70363
147 106 3.1 659 2 A64228
148 106 3.1 1291 2 A49777
149 106 3.1 1291 2 S46431
150 106 3.1 2077 2 T44178

ALIGNMENTS

RESULT 1
I39811
Parasporal crystal protein cry3Bb1 - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIIIb2
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39811
R;Donovan, W.P.; Rupa, M.J.; Slaney, A.C.; Malvar, T.; Gawron-Burks, M.C.; Johnson, T.H
Appl. Environ. Microbiol. 58, 3921-3927, 1992
A;Title: Characterization of two genes encoding Bacillus thuringiensis insecticidal crys
A;Reference number: I39811; MUID:93119147; PMID:1476436
A;Accession: I39811
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-652 <RES>
A;Cross-references: UNIPROT:Q06117; GB:M89794; NID:g142729; PIDN:AAA22334.1; PID:g142730
C;Genetics:
A;Gene: cryIIIB2
C;Superfamily: parasporal crystal protein

Query Match 100.0%; Score 3406; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.1e-210;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPNNRSEHDTIKVTPNSELTQTNHNPVLADNPNSTLEELNYKEFLRMTSDSSTEVLDNS 60
Db 1 MNPNNRSEHDTIKVTPNSELTQTNHNPVLADNPNSTLEELNYKEFLRMTSDSSTEVLDNS 60
Qy 61 TVKDAVGTGISVVGQILGVGVPPAGALTTFYQSFLNTIWPSSDADPWKAFMAQVEVLIDK 120
Db 61 TVKDAVGTGISVVGQILGVGVPPAGALTTFYQSFLNTIWPSSDADPWKAFMAQVEVLIDK 120
Qy 121 KIEYAKSKALAEQGLQNNPEDIYVNALNSWKKTPLSIRSKRSQDRIRELFSQAESFRN 180
Db 121 KIEYAKSKALAEQGLQNNPEDIYVNALNSWKKTPLSIRSKRSQDRIRELFSQAESFRN 180
Qy 181 SMPFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGGEWGYSSDVAEFYHRQLKLTQY 240
Db 181 SMPFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGGEWGYSSDVAEFYHRQLKLTQY 240
Qy 241 TDHCNNYVNLGLRGSTYDAWVKFRFRREMTLTVLDLVLFPFYDIRLYSGVKTEL 300
Db 241 TDHCNNYVNLGLRGSTYDAWVKFRFRREMTLTVLDLVLFPFYDIRLYSGVKTEL 300
Qy 301 TRDIFTDPIFSLNTLOEYGPFTFLSIENSIRKPHLFDYLQIEFTRTLQPGYFGKDSFNW 360
Db 301 TRDIFTDPIFSLNTLOEYGPFTFLSIENSIRKPHLFDYLQIEFTRTLQPGYFGKDSFNW 360
Qy 361 SGNVETRPSIGSKTTITSPFYGDKSTPEPVOKLSFDQKQVYRTTANTDVAAMPNGKVYL 420
Db 361 SGNVETRPSIGSKTTITSPFYGDKSTPEPVOKLSFDQKQVYRTTANTDVAAMPNGKVYL 420
Qy 421 VTKVDFSQYDDQKNETSTQTYDSKRNNGHVSQAQSIDQLPETTDEPLEKAYSQNLNVAE 480
Db 421 VTKVDFSQYDDQKNETSTQTYDSKRNNGHVSQAQSIDQLPETTDEPLEKAYSQNLNVAE 480
Qy 481 CFLMQDRGTIPFTTWTHTSRSDVFNTIDAETITQLPVVKAYALSSGASIIEGPGFTGNL 540
Db 481 CFLMQDRGTIPFTTWTHTSRSDVFNTIDAETITQLPVVKAYALSSGASIIEGPGFTGNL 540
Qy 541 LFLKESNSIAKFKVTLNSAALLQRYRIRYASTTNLRFLVQNSNNDFLVIYINKTNWK 600
Db 541 LFLKESNSIAKFKVTLNSAALLQRYRIRYASTTNLRFLVQNSNNDFLVIYINKTNWK 600
Qy 601 DDDLTQYTFDLATTNSNMGFSQDKNELIIGAESFVSNEKIYIDKIEFIPVQL 652
Db 601 DDDLTQYTFDLATTNSNMGFSQDKNELIIGAESFVSNEKIYIDKIEFIPVQL 652

RESULT 2

S10228
parasporal crystal protein cry3Ba1 - Bacillus thuringiensis (fragment)
N;Alternate names: coleopteran-active parasporal crystal protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S10228
R;Sick, A.; Gaertner, P.; Wong, A.
Nucleic Acids Res. 18, 1305, 1990
A;Title: Nucleotide sequence of a coleopteran-active toxin gene from a new isolate of Bac
A;Reference number: S10228; MUID:90206811; PMID:2320431
A;Accession: S10228
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-659 <SIC>
A;Cross-references: UNIPROT:P17969; EMBL:X17123; NID:g40258; PIDN:CAA34983.1; PID:g40259
C;Genetics:
A;Gene: cryIIIB
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin; toxin
Query Match 94.3%; Score 3212; DB 2; Length 659;
Best Local Similarity 93.7%; Pred. No. 8.2e-198;
Matches 610; Conservative 22; Mismatches 19; Indels 0; Gaps 0;


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QY 241 TDHCYNNVNGLNGRSGTSDAWKFNFREREMTLTVLDLVLPPFYDIRLYSGVKTEL 300
Db 248 TDHCYNNVNGLNGRSGTSDAWKFNFREREMTLTVLDLVLPPFYDIRLYSGVKTEL 307
QY 301 TRDIPTDPIFSLNTLOEQYGPFTLSIENSIRKPHLDYLOGLIEFHTRLOQYGVGKDSFNW 360
Db 308 TRDVLTPDIVGNNLRGVTFTSNIENIRKPHLDYLOGLIEFHTRLOQYGVGKDSFNW 367
QY 361 SGNVETRPSIGSSKTIIPFFYGDKSTEPVQKLSFDGQKVYRTTANTDVAAPNGKVVYG 420
Db 368 SGNVSTRPSIGSDIITSPPFYGNKSSBPVQNFENGKVRANVTNLAWP6A-VYSG 426
QY 421 VTKVDFSQDDOKNETSTQYDSKNNNGHVSQAQSDIDQLPPTTDEPLEKAYSHQNLAYE 480
Db 427 VTKVDFSQDDOKNETSTQYDSKNNNGHVSQAQSDIDQLPPTTDEPLEKAYSHQNLAYE 485
QY 481 CFMLQDRRGTIPFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGTGNL 540
Db 486 CFMLQDRRGTIPFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGTGNL 545
QY 541 LFLKSSNSIAKFKVTLNSAALLQRYVRIRVASTTNLRLFVQNSNDFLVIYINKTMNK 600
Db 546 IQCTE-NGSAATYVTPDVSYSQKTRARIHASTSQITFTLSLDGAPNQYFPKTKNK 603
QY 601 DDDLTQYQTFDLATTNSNMFGSGDKNELIIGAESFVSNKIEYIDKIEFIPV 650
Db 604 GDTLTYSNLAESFSPFELSG--NNLQIGVTGLSAGDKVYIDKIEFIPV 651

RESULT 4
JH0261
paraasporal crystal protein cry3Cal - Bacillus thuringiensis subsp. kurstaki (strain BT11)
N:Alternate names: paraasporal crystal protein cryIIID
C:Species: Bacillus thuringiensis subsp. kurstaki
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JH0261; S18944
R:Lambert, B.; Theunis, W.; Aguda, R.; Van Audenhove, K.; Decock, C.; Janssens, S.; Seuri
Gene 110, 131-132, 1992
A:Title: Nucleotide sequence of gene cryIIID encoding a novel coleopteran-active crystal
A:Reference number: JH0261; MUID:92184108; PMID:1544571
A:Molecule type: DNA
A:Residues: 1-649 <LAM>
A:Cross-references: UNIPROT:Q45744; EMBL:X59797; NID:g40287; PIDN:CAA42469.1; PID:g40288
C:Genetics:
C:Superfamily: paraasporal crystal protein

Query Match 63.2%; Score 2152; DB 1; Length 649;
Best Local Similarity 62.2%; Pred. No. 5.6e-130; Indels 10; Gaps 6;
Matches 407; Conservative 95; Mismatches 142;

QY 1 MNPNNRSHDTIKVTPNSELOTNHNQYPLADNPNTLEELNYKEFLRMTESSSTEVLDS 60
Db 1 MNPNNRSHDTIKATENNEVSNHAQYPLADTP--TLEELNYKEFLRTTDDNNVEALDSS 58
QY 61 TVKDAVGTGISVVGQILGVVGPFGALTSFYQSFLNTIWPSSDADPWKAFMAQVEVLIDK 120
Db 59 TTKDAIQKGIISIGDGLLVGVPYGGALVSFYTNLLNTIWPGE--DPLKAFMQQVEALIDQ 117
QY 121 KIEEYAKSKALAELOGLNNEFDYNNALNSWKTKPLSLRSKRSDRIREFLSQAESHFRN 180
Db 118 KIADYAKDKATAELOGLNKVFADYVSLDSDWDKPTPLTRDGRSSQGRIRREFLSQAESHFR 177
QY 181 SMPSPAVSKFEVLFPLTYQAANTHLLLLKDAQVFGGEWGSVSDAEFFHTRQLKLTQY 240
Db 178 SMPSPAVSGEYVLFPLTYQAANTHLLLLKDAQYIGTDGYSSTDLENEFHTKQDLTIEY 237
QY 241 TDHCYNNVNGLNGRSGTSDAWKFNFREREMTLTVLDLVLPPFYDIRLYSGVKTEL 300
Db 238 TNHCAKWKAGLDKLRGTYEAWKFNFREREMTLTVLDLVLPPFYDIRLYSGVKTEL 297
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QY 301 TRDIPTDPIFSLNTLOEQYGPFTLSIENSIRKPHLDYLOGLIEFHTRLOQYGVGKDSFNW 360
Db 298 TRDVLTPDIVANNMNGYGTFTSNIENIRKPHLDYLOGLIEFHTRLOQYGVGKDSFNW 357
QY 361 SGNVETRPSIGSSKTIIPFFYGDKSTEPVQKLSFDGQKVYRTTANTDVAAPNG----K 416
Db 358 SGNVSTRPSIGSDEIIRSPFYGNKSTLDVQNFENGKVRANVTNLAWP6VGTGGTK 417
QY 417 VILGVTKVDFSQDDOKNETSTQYDSKNNNGHVSQAQSDIDQLPPTTDEPLEKAYSHQL 476
Db 418 IHSGVTKVDFSQDDOKNETSTQYDSKNNNGHVSQAQSDIDQLPPTTDEPLEKAYSHQL 476
QY 477 NYAECLFMQDRRGTIPFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGT 536
Db 477 NYVRCLFMQDRRGTIPFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGT 536
QY 537 GGNLLFLKSSNSIAKFKVTLNSAALLQRYVRIRVASTTNLRLFVQNSNDFLVIYINK 596
Db 537 GGDIKCTNGS--GLTLYVTPADLTYSKYIRVASTSQVRFGLDLSYTHSISYFDK 595
QY 597 TMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESFVSNKIEYIDKIEFIPV 650
Db 596 TMDKNTLTYSNLSVSRPIEISGG--NKIGVSGVGGIGSDEYIDKIEFIPV 648

RESULT 5
S49247
paraasporal crystal protein cry3Cal [validated] - Bacillus thuringiensis
N:Alternate names: paraasporal crystal protein cryIH
C:Species: Bacillus thuringiensis
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A59350; S49247
R:Lambert, B.; Buyse, L.; Decock, C.; Janssens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
Appl. Environ. Microbiol. 62, 80-86, 1996
A:Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agair
A:Reference number: A59350; MUID:96141404; PMID:8527215
A:Accession: A59350
A:Molecule type: DNA
A:Residues: 1-1157 <LAM>
A:Cross-references: UNIPROT:Q45733; EMBL:Z37527; NID:g547554; PIDN:CAA85764.1; PID:g54757
A:Experimental source: serovar tolworthi
A:Comment: This paraasporal crystal protein, active against corn borer and other insects,
C:Superfamily: paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 33.1%; Score 1127.5; DB 1; Length 1157;
Best Local Similarity 36.1%; Pred. No. 4.8e-64;
Matches 250; Conservative 148; Mismatches 217; Indels 77; Gaps 19;

QY 1 MNPNNRSHDTIKVTPNSELOTNHN--QYPLADNPNTLEELNYKEFLRMTESSSTEVLDS 59
Db 1 MNPNNRSHDTIKVTPNSELOTNHN--QYPLADNPNTLEELNYKEFLRMTESSSTEVLDS 59
QY 60 STV----KDAVGTGISVVGQILGVVGPFGALTSFYQSFLNTIWP--SDADPWKAFMAQV 114
Db 60 PSLISGRDAVQATLTVVGRILGALGVPSQIYFYQFLNTLTLPVNDTALWEAFMQV 119
QY 115 EYLIDKIEEYAKSKALAELOGLNNEFDYNNALNSWKTKPLSLRS--KRSQDRIRLEFSQ 173
Db 120 EELVNCQITEFARNQALRLQGLGDSFNRYQSLQNW----LADNDRTNLSVVAQAFIA 175
QY 174 ASHFNRNMPSPAVSKFEVLFPLTYQAANTHLLLLKDAQVFGGEWGSVSDAEFFHTRQ 233
Db 176 LBLDFVNAIPLFAVNGQQVPLLSVYAQAANLHLLLLKDAQVFGGEWGSVSDAEFFHTRQ 235
QY 234 LKLTQYTDHCVNNVNGLNGRSGTSDAWKFNFREREMTLTVLDLVLPPFYDIRLYS 293
Db 236 LETAKYTNVCEWYNTGLDRLRGNTESWLRHYQFRREMTLVLDVVAALFPYDVRYP 295
QY 294 KGKTELTDRDIFTDPIF-----SLNTLOEQYGP-----TFLSIENS--IRKPHLDYLOGLIE 343
Db 296 TGSNPQLTREVTDPITVFNPANVGLCRWGTNPNYTFSELENAFIRPPLFDRLNLSLT 355
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349 PGYFGKDSFNWYSGNYVETRSIGSSKTIITSPFFYGDKSTPEVQK--LSFDGQKVYRTIAN 406
 348 PDLF-----YWSAHKVSFKS-EQSNLYTTGTIYG-KTSGYISSGAYFSGNDIYRTILAA 399
 407 TDVAAPNGKVLGVTKVDFESQYDDQKNETSTQTVYDSKRNGHVSQAQSDIDQLPETTDE 466
 400 PSVVVYPTONT-GEQVEFVGKGVHVRGDKVD-----LTVDSIDQLPPD--GE 448
 467 PLEKAYSHQNYAECLFMQD---RRGTIPFTWTHRSVDFPNTTDAEKITOLPVKAYAL 523
 449 PIHEKYTHLCHATAIFKSTPDYDNATIPISWTHRSAYEYNNRYPNNKTIKIPAVKMYKL 508
 524 SGASIIIEGPGTGNLLFLKSSNSIAKFVTLNSAALLQRYVRIRIYASTTNLRLFLVQ 583
 509 DDPSTVVGPGTGGDLV-KRGSTGVIGDIKATVNS-PLSQYRVRYAT----- 557
 584 NSNNDPLVIYN-----KTMNKDDLTQYTFDLATNNSMFGSGDKNELIIG 630
 558 NVSGQFNW-YINDKITLQTKFQNTVETIGEGKDLTVSGFYIEYSTTIQFPDEHPKITLH 616
 631 AESFVNEKIYDKIEFIPVQL 652
 617 LSDLSNNSFYVDSIEFIPVDV 638

RESULT 8
 I39815
 insecticidal protein cryv - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I39815
 R:Gleave, A.P.; Williams, R.; Hedges, R.J.
 Appl. Environ. Microbiol. 59, 1683-1687, 1993
 A:Title: Screening by polymerase chain reaction of Bacillus thuringiensis serotypes for
 iensis subsp. kurstaki.
 A:Reference number: I39815; MUID:93298009; PMID:8517758
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <RES>
 A:Cross-references: UNIPROT:Q45752; GB:M98544; NID:g142767; PIDN:AAA22354.1; PID:g142768
 C:Genetics:
 A:Gene: cryv
 C:Superfamily: parasporal crystal protein

Query Match 32.3%; Score 1100.5; DB 2; Length 719;
 Best Local Similarity 36.6%; Pred. No. 1.3e-62;
 Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNPSELQTNHNPYPLADNPSTLEELNYKEFLRMTESS 53
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKMSYEY 50
 QY 54 TE-VLDNSTVTKDAVGTGIVSVGOILGVVGPFGAGALTSTFYQSFNTIWPSPDADPWKAFMA 112
 DB 51 VEPFVSASTIQ-----TGIGIAGKILGTGVPAGQVASYLFGELWPKGKQWEIFME 106
 QY 113 QVEVLIDKKIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKSDRIELFS 172
 DB 107 HVEEIIQKISTYARNKALTDLGLGDALAVVHDSLESVWG---NRNTRARSVVKSQYI 163
 QY 173 QAESHPNRMSPFSAVSKPEVLPLPYAQAANTHLLLLKDAQVFGEGWYSSYEDVAEFYHR 232
 DB 164 ALELMFVQKLPFAVSGEVPPLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFVNR 223
 QY 233 QLKLTQOYTDHCVNWNVNGLGRSTYDAWKFNRFREMTLTVLDLIVLPFPDYRLY 292
 DB 224 QVERAGDYSCHVKWYSTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQY 283
 QY 293 SKGVKTELTRDIFTD-----PIFSLNT-LQEVGPTPLSTENS-IRKPHLFDYLOGIE 342
 DB 284 PIKTTAQLTRVYDAIGTVHPHPSFTSTTWNNNAPSFSALEAAVVRNPHLLDLEQVT 343

343 FHTRLQPGYFGKDSFNWYSGNYVETRSIGSSKTIITSPFFYGDKSTPEVQKLSFDGQKVYR 402
 344 IYSLLS-RWSNTQYNNMNGHKLBEFR-TIGTGLNISTOGSTNTSINPV-TLPFTSRDVR 400
 403 TITANTDVAAPNGKVLGVTKVDFESQYDDQKNETSTQTVYDSKRNGH-----VSAQSDIDQ 458
 401 TESLAGLNLFLTQPNV-GVPRVDF---HWKFVTHPIASDNFYYPGVAGIGTQLQDSENE 455
 459 LPPETTTDEPLEKAYSHQNYAECLFMQDQRRGTIPFTWTHRSVDFPNTTDAEKITOLPVV 518
 456 LPEATGQPNVESYSHRLSHIGLSASHVKALV--YSWTHRSADRTNIENTSPSIQIPLV 513
 519 KAYALSSGASIIIEGPGTGNLLFLKSSNSIAKFVTLNSAALLQRYVRIRIYASTTNL 578
 514 KAPNLSGGAUVKPGPTGGDIL-RTWTGTGDIRVIN-PPFAQRYVRIRIYASTTDL 571
 579 RLFLVQ-----NSNNDPLVIYNKMKDDDLTYQTFDLATNNSMFGSGDKNELIIGAE 632
 572 QFHTSINGKAIQGN-----FSATMNRGEDLDYKTFRTVGTTPFSLDVGOSTFTIGAW 625
 633 SFVSNKIIYDKIEFIPVQL 652
 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 9
 I39814
 insecticidal protein cryv1 - Bacillus thuringiensis
 C:Species: Bacillus thuringiensis
 C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 26-Aug-1999
 C:Accession: I39814
 R:Shin, B.S.; Park, S.H.; Choi, S.K.; Koo, B.T.; Lee, S.T.; Kim, J.I.
 Appl. Environ. Microbiol. 61, 2402-2407, 1995
 A:Title: Distribution of cryv-type insecticidal protein genes in Bacillus thuringiensis
 tomoscidus.
 A:Reference number: I39814; MUID:95314293; PMID:7793960
 A:Accession: I39814
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-719 <RES>
 A:Cross-references: GB:L36338; NID:g540281; PIDN:AAC36999.1; PID:g540282
 C:Genetics:
 A:Gene: cryv1
 C:Superfamily: parasporal crystal protein

Query Match 32.0%; Score 1091.5; DB 2; Length 719;
 Best Local Similarity 36.5%; Pred. No. 4.9e-62;
 Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNPSELQTNHNPYPLADNPSTLEELNYKEFLRMTESS 53
 DB 1 MKLKNQDKHQSFSSNAKVDKISTDS-----LKNETDIELQNIHEDCLKMSYEY 50
 QY 54 TE-VLDNSTVTKDAVGTGIVSVGOILGVVGPFGAGALTSTFYQSFNTIWPSPDADPWKAFMA 112
 DB 51 VEPFVSASTIQ-----TGIGIAGKILGTGVPAGQVASYLFGELWPKGKQWEIFME 106
 QY 113 QVEVLIDKKIEYAKSKALAELOGLQNNFEDYVNALNSWKKTPLSLRSKSDRIELFS 172
 DB 107 HVEEIIQKISTYARNKALTDLGLGDALAVVHDSLESVWG---NRNTRARSVVKSQYI 163
 QY 173 QAESHPNRMSPFSAVSKPEVLPLPYAQAANTHLLLLKDAQVFGEGWYSSYEDVAEFYHR 232
 DB 164 ALELMFVQKLPFAVSGEVPPLPIYAQAANLHLLLLRDASIFGKEWGLSSSEISTFVNR 223
 QY 233 QLKLTQOYTDHCVNWNVNGLGRSTYDAWKFNRFREMTLTVLDLIVLPFPDYRLY 292
 DB 224 QVERAGDYSCHVKWYSTGLNLRGTNAESWRYNQFRDMTLMVLDLVALFPSTQY 283
 QY 293 SKGVKTELTRDIFTD-----PIFSLNT-LQEVGPTPLSTENS-IRKPHLFDYLOGIE 342
 DB 284 PIKTTAQLTRVYDAIGTVHPHPSFTSTTWNNNAPSFSALEAAVVRNPHLLDLEQVT 343

QY 343 FHTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKTTITSPFYGDKSTEPVQKLSFDGOKVYR 402
Db 344 IYSLLS-RWNTQYMMWGMGHKLEFR-TIGTLNISTQGSTNTSINPV-TLPFTSRDVR 400
QY 403 TIANTDVAAMPNGKVYLGVTQKDFPSQYDDOKNETSTQYDSKRNNGH-----VSAQDSIDQ 458
Db 401 TESLAGLNLFLTQPVN-GVPRVDF-----HWKFVTHPIASDNFYYPGVAGIGTQLQDSENE 455
QY 459 LPPEITDEPLEKAYSHQNLVAECFLMQDRGTIPFFFTWTHRSVDFNTDAEKITQLPVV 518
Db 456 LPEATQPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNISITQIPLV 513
QY 519 KAYALSSGASIIIGPGFTGNNLLFLKESNSIAKFVKTLNSAALLQRYRVRIRYASTTNL 578
Db 514 KAFNLSSGAAVRPGFTGDDIL-RRNTGTFGDIRVIN-PFPAQRYRVRIRYASTTDL 571
QY 579 RLFPVQ-----NSNNDPLVIYINKTMKODDLTYQTDFLATNNSMGFSGDKNELIGAE 632
Db 572 QPHTSINGKAINQGN-----FSATMNRGSDLDYKTFRTVGFTTTPFSFLDVQSTFTIGAW 625
QY 633 SFVSNKIIYDKIEFIPVQL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 10
S25383
paraesporal crystal protein cryIIa1 - Bacillus thuringiensis
N;Alternate names: delta-endotoxin; paraesporal crystal protein cryII
C;Species: Bacillus thuringiensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S25383
R;Tailor, R.; Tippett, J.; Gibb, G.; Pells, S.; Pike, D.; Jordan, L.; Ely, S.
Mol. Microbiol. 6, 1211-1217, 1992
A;Title: Identification and characterization of a novel Bacillus thuringiensis delta-end
A;Reference number: S25383; MUID:92269582; PMID:1588820
A;Accession: S25383
A;Molecule type: DNA
A;Residues: 1-719 <TAI>
A;Cross-references: UNIPROT:Q45752; EMBL:X62821; NID:g40289; PIDN:CAA44633.1; PID:g40290
C;Genetics:
A;Gene: cryII
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 32.0%; Score 1091.5; DB 2; Length 719;
Best Local Similarity 36.5%; Pred. No. 4.9e-62;
Matches 248; Conservative 137; Mismatches 232; Indels 63; Gaps 19;

QY 1 MNPNNRSEHDTI-----KVTNSELQTNHNOYPLADNPSTLEELNYKEFLRMTESS 53
Db 1 MKLKNQDKQSFSSNAKVDKISTDS-----LKNETDIELQNHEDCLMKSEYEN 50
QY 54 TE-VLDNSTKDAVGTGIVGVGQILGVGVGPGAGALTSPYQSFINTIPFSDADPWKAFMA 112
Db 51 VEPFVSASTIQ-----TGIGIAGKILGTGLGVFAGQVASYLSFTLGEMLPKGKQWEIFME 106
QY 113 QVEVLDKKIEEYAKSALAELOGLQNNFEDYVNALNSKKTPLSLRKSRQDRIBELFS 172
Db 107 HVBEIINQKISTYARNKALTDLKGLGDALAVYHDSLESVWG-----NNNTRARSVKSQYI 163
QY 173 QAESHFERNMPSFAVSKFVLPLPTVAQAANTHLLLLKDAQVFGSEWGYSSDEVAEFYHR 232
Db 164 ALELMFVQKLPSFAVSGEEVPLPIYIAQAANLHLLLRDASIPGKEWGLSSSEISTFYNR 223
QY 233 QKLKLTQYTDHCVNWNVNGLNGRGSTYDAWVKFNPRFRREMTLTVLVDLVLFPFFYDIRLY 292
Db 224 QVERAGDYSVHCVKWYSTGLNLRGTAESWVRYNQFRDMLTDLVLVLPFSDYQY 283
QY 293 SKGVKTELTRDITD-----PIFLNT-LOEYGPFTLSIENS-IRKPHLFDYLOQIE 342
Db 284 PIKTTAQLTREYVDAIGTVHPPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLIDLEQVT 343

QY 343 FHTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKTTITSPFYGDKSTEPVQKLSFDGOKVYR 402
Db 344 IYSLLS-RWNTQYMMWGMGHKLEFR-TIGTLNISTQGSTNTSINPV-TLPFTSRDVR 400
QY 403 TIANTDVAAMPNGKVYLGVTQKDFPSQYDDOKNETSTQYDSKRNNGH-----VSAQDSIDQ 458
Db 401 TESLAGLNLFLTQPVN-GVPRVDF-----HWKFVTHPIASDNFYYPGVAGIGTQLQDSENE 455
QY 459 LPPEITDEPLEKAYSHQNLVAECFLMQDRGTIPFFFTWTHRSVDFNTDAEKITQLPVV 518
Db 456 LPEATQPNYESYSHRLSHIGLISASHVKALV--YSWTHRSADRTNTIEPNISITQIPLV 513
QY 519 KAYALSSGASIIIGPGFTGNNLLFLKESNSIAKFVKTLNSAALLQRYRVRIRYASTTNL 578
Db 514 KAFNLSSGAAVRPGFTGDDIL-RRNTGTFGDIRVIN-PFPAQRYRVRIRYASTTDL 571
QY 579 RLFPVQ-----NSNNDPLVIYINKTMKODDLTYQTDFLATNNSMGFSGDKNELIGAE 632
Db 572 QPHTSINGKAINQGN-----FSATMNRGSDLDYKTFRTVGFTTTPFSFLDVQSTFTIGAW 625
QY 633 SFVSNKIIYDKIEFIPVQL 652
Db 626 NFSSGNEVYIDRIEFVPEV 645

RESULT 11
S00873
paraesporal crystal protein cryBa1 - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: paraesporal crystal protein cryA4
C;Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S00873
R;Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2733-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus t
A;Reference number: S00873; MUID:88203216; PMID:3362680
A;Accession: S00873
A;Molecule type: DNA
A;Residues: 1-1228 <BRI>
A;Cross-references: UNIPROT:P05517; EMBL:X06711; NID:g40264; PIDN:CAA39898.1; PID:g58094
C;Genetics:
A;Gene: cryA4
A;Start codon: TTG
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 31.5%; Score 1072.5; DB 2; Length 1228;
Best Local Similarity 36.6%; Pred. No. 1.7e-60;
Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;

QY 1 MNPNNRSEHDTI-KVTNSELQTNHNOYPLADNPSTLEELNYKEFLRMTESSSTEVLDNS 60
Db 1 MTSNRKNEEIIINAVSNHSAQMD-----LLPDARIEDSLCIAEGNN---IDPF 45
QY 61 TVKDAVGTGIVGVGQILGVGVGPGAGALTSPYQSFINTIPFSDADPWKAFMAQVEVLIDK 120
Db 46 VSASTVQTGINTAGRILGVGVFAGQLASFTSFLVGEMLWPRGRDQWELFLEHVEQLNQ 105
QY 121 KIEEYAKSALAELOGLQNNFEDYVNALNSKKTPLSLRKSRQDRIRE-LFSQ---AES 176
Db 106 QITENARNLTALRLQGLGSPRAYQGSLEDWLE-----NRDDARTSRVLYTYQIALEL 158
QY 177 HFRNSMPSFAVSKFVLPLPTVAQAANTHLLLLKDAQVFGSEWGYSSDEVAEYHRLQKL 236
Db 159 DFLNAMPLFAIRNQSEVPLLMVYAQAANLHLLLRDASLFGSFGSLTSQSIQRYRQVER 218
QY 237 TQOYTDHCVNWNVNGLNGRGSTYDAWVKFNPRFRREMTLTVLVDLVLFPFFYDIRLSKGV 296
Db 219 TRDYSDYCVENWTGLNLSRGTAESWVRYNQFRDMLTGLVDLVALFPSYDTRTPINT 278
QY 297 KTELTRDITDPI-----FSLNTLQBYGPTFLSIE-NSIRKPHLFDYLOQIEFHTRLQ 348
Db 284 PIKTTAQLTREYVDAIGTVHPPHPSFTSTTWNNNAPSFSAIEAAVVRNPHLLIDLEQVT 343

Db 279 SAQLTREVVYDAIGATGVNMAWMNNYNNAPSFAIEAAAIRSPHLLDFLEQLTIFS-AS 337
Qy 349 POYFGKDSFNWNGYVETRPSIGSSKITSPFYG--DKSTPEVQKLSFDGQKVYRIAN 406
Db 338 SRWNSRTHMYWRIGHTIOSRPTGGGLNST--HGATNTSINPV-TLPASRDVRYTESY 393
Qy 407 TDVAAPNGKVYL----GVTKVDFQYDDQK-NETSTQTYDSKRNNGHVSAQDSIDLPP 461
Db 394 AGVLLW---GIVLEPIHGVPVTRFNTPNQNISDRGTANYSQPYESPGQLQKDSLETLP 450
Qy 462 ETTDPLEKAYSHQNLNVAECFLMDRRGTIPFFTWTHRSVDFNTIDAETITOLPVVKAY 521
Db 451 ETTERPNVESHRLSHIGIILQSS--RVNVPYVSWTHRSADRTNTIGNRITQIPMWKAS 508
Qy 522 ALSSGASIEEGPFTGGNLLFKESNSIAKPKVTLNSAALLQRYRVRIRYASTTNLRLF 581
Db 509 ELPOGFTVVRGPGFTGGDIL-RTWGGPGPRVTVN-GPLTORVIGFRVASTVDPDF 566
Qy 582 VQNSN---NDFLVIYINKTMKDDDLTYOTFDLATNNSMGSGDKNELIIGAESFVUNE 638
Db 567 VSRGGTTVNNRFL---RTMNGDELKYGNFVRRAPTTPFTTQIQDIIRTSIQLSGNG 623
Qy 639 KIYIDKIEPIPV 650
Db 624 EYVIDKIEIIPV 635

RESULT 12
I40589
parasporal crystal protein cry8Cal - Bacillus thuringiensis
N;Alternate names: parasporal crystal protein cryIII
C;Species: Bacillus thuringiensis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40589
R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami, M.; Kaji, Y.; Suzuki, N.; Hori, H.; Asano
Curr. Microbiol. 28, 15-19, 1994
A;Title: Cloning, heterologous expression, and localization of a novel crystal protein g
A;Reference number: I40589; MUID:94100786; PMID:7764305
A;Accession: I40589
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-1160 <RES>
A;Cross-references: UNIPROT:Q45706; EMBL:U04366; NID:g532523; PIDN:AAA21119.1; PID:g5325
A;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 31.1%; Score 1060; DB 2; Length 1160;
Best Local Similarity 37.1%; Pred. No. 1e-59;
Matches 254; Conservative 116; Mismatches 254; Indels 60; Gaps 21;

Qy 1 MNPNNRSEHTIKVTPNSELOTHNQYPLADNPNSTILEELNYKEFLMTEDSSTEVLDS 60
Db 1 MSPNNQNEYIIDLSPSVSDNSIRYPLANDQNTLQNNYKDYLKMTSTNAELSRNP 60
Qy 61 ----TVKDAGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIWPSS--DADPWKAFMAQVE 115
Db 61 GTFISAQAVGTGIDIVSTTISGLGIPVLGEVFSILGSLGLMPNSNENVMQIFNWRVE 120
Qy 116 VLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKTPLSURSKRSQDRIRBELFSQAE 175
Db 121 ELIDQKILDSVRSRAIDLANSRIAIVEYQNALEDWRKNP---HSTRSAALVKERFGNAE 177
Qy 176 SHFNNSMPSFAVSKEFVLFLPTAQAAANTHLLKDAQVGEWGSYSDVAEFYHRLK 235
Db 178 AILRTNMGFSQTYETPLPLPTAQAAASHLLVNRDQVIYKEGWYQNDIDILFYKEQVS 237
Qy 236 LTOQYTHCVNMYNGLNGRSTYDAWVKFNFREREMTLTVLDLIVLFPFYDIRLYSKG 295
Db 238 YTARYSDCHVQYVYAGNLKLAGTGAKQWVDYNNFREREMVNVLDLVALFNYDARIYPLE 297
Qy 296 VKTELTRDITDTPISLNTLQE-----YG-----PTFLSIENSIRKPHLFDVLOGIEF 343
Db 298 TNAELTREIFDTPGVSYVTGQSSSTLISWYDMIPALPFSFSTLENLLRKRDPFTLLQELRM 357

Qy 344 HTRL-OPGVFGKDSFNWNGYVETRPSIGSS-KTITSPPFYGDKSTPEVQKLSFDGQK-V 400
Db 358 YTSFRONGTI--EYNYWGGQRLTLSYIYGSSFNKYSGVLGAEDIIIPV-----QNDI 409
Qy 401 YRTIANTDVAAMPNGKVGILGVTKVDFSQYDDQKNETSTQTYDS-KRNNGHVSAQDSIDL 459
Db 410 YRVVW-TYIGRYTNS--LLGVNPTF-----YFSNNTQKTSYKPKQFAGGIKIDSGEEL 461
Qy 460 PPETDDEPLEKAYSHQNLNVAECFLMDRRGT-----IPFTWTHRSVDFNTIDAETITOL 515
Db 462 TYEN-----YQSYSHRVSYITSFEIKSTGCTGLGVGVPIFGWTHSSASRNNFIYATKISQI 516
Qy 516 PVVKAYALSGA--SIEEGPFTGGNLLFKESNSIAKPKVTLNSAALLQRYRVRIRYA 573
Db 517 PINKASRTSGAVNWFQEG-L-YNGGPMVKSLSGSGSVQINLRVATDAKASQRYRIRYA 575
Qy 574 S-----TTNLRFLVQNSNNDFLVIYINKTMKDDDLTYOTFDLATNNS-NMGFSGDKNE 626
Db 576 SDRAGKFTISSRSPENPATYSASIAVTN-TMSTNASLTSTPAYAESGPINLGISGSR 634
Qy 627 LIIGAESFVNEKIIYDKIEPIPV 650
Db 635 FDISITKEAGAANLYIDRIEFIPV 658

RESULT 13
S39536
parasporal crystal protein cry9Ba1 - Bacillus thuringiensis
N;Alternate names: Delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepan
FBIS Lett. 336, 79-82, 1993
A;Title: Primary structure of the cryX, the novel delta-endotoxin-related gene from Bacil
A;Reference number: S39536; MUID:94085596; PMID:8262221
A;Accession: S39536
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: UNIPROT:Q45745; EMBL:X75019
A;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 28.3%; Score 963.5; DB 2; Length 1154;
Best Local Similarity 33.3%; Pred. No. 1.5e-53;
Matches 214; Conservative 135; Mismatches 243; Indels 51; Gaps 16;

Qy 41 NYKEFLRMT-DSSTEVLDNSTVDAGVTGTSVVGQILGVVGVFPAGALTSFYQSFLNTI 99
Db 29 SYKDYLKMSGDIYDSYINPGNVRTGLQTGIDIVAVVVGALGPGVGGILTGLSLFGFL 88
Qy 100 WPS-DADPWKAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKTKPLSL 158
Db 89 WPSNDQAVWEAPTEQMEELIEQIRISDQVVRALDLDLTGIONYYQYLIALKWEERPNV 148
Qy 159 RSKRSQDRIRELFSQAESHFRNSMPSPF-----AVSKFEVLFLPTAQAAANTHLLKDAQV 214
Db 149 RA-----NLVLQRFELHALFVSSMPSFGSGPQSRFOAQLLVVYAAANLHLLADAEK 204
Qy 215 FQEEWGYSSDVAEFYHRLK-L-TQOYTHCVNMYNGLNGRSTYDAWVKFNFRREM 273
Db 205 YGARWGLRESQGLNYFNELOTRTRDYTNHCVNMYNGLNGRSTYDAWVKFNFRREM 264
Qy 274 TLTVLDLIVLFPFYDIRLYSKGKTELTDRIDFTDP-----IFSLNTLQEVGP 320
Db 265 TLMAMDILALFPYVNTRRPIAVNPQLIREVYTDPLGVSESSLPPELRLCRLWQETSAN 324
Qy 321 TFLSIENS-IRKPHLFDYLOGIEFHTRLQPGVFGKDSFNWNGYVETRPSIGSSKITFS 379
Db 325 TFSNLENAIISPHLPDITNNLMIVTGSFVSHLTNQLIEGWIGHSVTSLLASGPTTVLR 384

Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434
Qy 485 QDRRGTIFF-----FTWTHRSVDFNTIDAEEKITQLPFWKAYALSSGASIIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSWTHRSATLNTIDPERINQIPLVKGRFVWGGSVITGPGFTGG 493
Qy 539 NLLFLKESNSIAKPKVTLSAALLQRYVRIRYASTTNLRLFV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYRLRFRYASSRDARVILVTGAAGTGVGGQVSVN 551
Qy 588 DELVIYINKTKNDDLLTYOTFDLATTNSNMGFS-----GDKNELIIGAESFVSNEKIY 641
Db 552 ----MPLQKTMEIGENLTSRTFRYDFSNPFSFRANPDIIGISEQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613
RESULT 16
S04181
parasporal crystal protein - Bacillus thuringiensis (strain aizawai 7.29) (fragment)
N:Alternate names: delta-endotoxin
C:Species: Bacillus thuringiensis
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04181
R:Sanchis, V.; Lereclus, D.; Menou, G.; Chaufaux, J.; Guo, S.; Lecadet, M.M.
Mol. Microbiol. 3, 229-238, 1989
A:Title: Nucleotide sequence and analysis of the N-terminal coding region of the Spodoptera frugiperda polyhedrin gene
A:Reference number: S04181, MUID:89343627; PMID:2548060
A:Accession: S04181
A:Molecule type: DNA
A:Residues: 1-823 <S>
A:Cross-references: UNIPROT:P05518; EMBL:X13620; NID:g40355; PIDN:CAA31951.1; PID:g40356
C:Genetics:
A:Gene: bta
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 26.6%; Score 907.5; DB 2; Length 823;
Best Local Similarity 35.8%; Pred. No. 3.5e-50;
Matches 239; Conservative 103; Mismatches 230; Indels 95; Gaps 27;
Qy 21 QTNHQ---YPLADNPSTLEELNYKEFLRMTESSSTEVLDN---STVKDVGTVGISVVG 74
Db 3 ENNQNCIPVNCUSNPEEVL-----LDGERISTGSSIDISLSLV- 42
Qy 75 QILGVGVPPAGALTSFYQSFLNTIWPSPADPWKAFMAQVEVLIDKKIEYAKSKALAE 134
Db 43 QFLVSNFVPGGFLVGLIDFVWGI VGPSQ---WDAFLVQIEQLINERIAEFARNAAIANL 99
Qy 135 QGLQNNFEDVYVNLNWKKTPLSLRSKRSQDRIRELFQSAESHFNSMPSFAVSKFELV 194
Db 100 EGLGNFNIEYAEKWEEDP---NNPATRVIDRFRILDGLLERDIPSFRTSGSEVPL 156
Qy 195 LPTVAQAAHLLLLDKDAQVFGREWGYSSEDAEFYHRQLKLTQQYTDHCVNWNVYVGLNG 254
Db 157 LSVTAQAAHLLALRLDSVIFGERWGLTTINVENYNLRIHIDEYADHCANYNRGLAN 216
Qy 255 LRGSSTDAWVKFRFRREMTLVLDLIVLPFFYDRIYLSKGVKTELTDRIDTPIPSLN- 313
Db 217 LPKSTYQDWITYNRLRDLTLVLDIAAFFPNYDNRYPPIQPVGQLTREYTDPLNFNP 276
Qy 314 TLQBYG--PFLSLTENS-IRKPHLFDYLQIEFHTRLPQGVFGKDSFNWYSGNYVETRPS 370
Db 277 QLQSVAGLPTFNWENSAIRNPHLFDILNLTPT-----DWFSVGRNFYWGHRVLS--S 330
Qy 371 IGSSKTTITSPYG-DKSTEPVKLSFDGQKQVYRT--IANTDVAAPNPKVYL---GVTKV 424
Db 331 LIGGNITSPYIGREANQEPSPFTFG-PVFRILTSIPTLRLLQQPCORHHFNLRGEGV 389
Qy 425 DFGSYDDQKNSTGTQYDYSKRNNGHVSAQSDIDQLPRTTDEPLEKAYSHQLYNAECFLM 484

Db 390 EFS-----TPTNSFTY---RGRGTV---DSLTELPPEDNSVPPREGYSHRLCHA---TF 434
Qy 485 QDRRGTIFF-----FTWTHRSVDFNTIDAEEKITQLPFWKAYALSSGASIIIEGPGFTGG 538
Db 435 VQRSGT-PFLTGTGVFSWTHRSATLNTIDPERINQIPLVKGRFVWGGSVITGPGFTGG 493
Qy 539 NLLFLKESNSIAKPKVTLSAALLQRYVRIRYASTTNLRLFV-----QNSNN 587
Db 494 DIL-RRNTFGDFVSLQVINS-PITQRYRLRFRYASSRDARVILVTGAAGTGVGGQVSVN 551
Qy 588 DELVIYINKTKNDDLLTYOTFDLATTNSNMGFS-----GDKNELIIGAESFVSNEKIY 641
Db 552 ----MPLQKTMEIGENLTSRTFRYDFSNPFSFRANPDIIGISEQPLFGAGS-ISSGELY 606
Qy 642 IDKIEFI 648
Db 607 IDKIEII 613
RESULT 17
S02134
parasporal crystal protein cryIC1 - Bacillus thuringiensis (strain aizawai IC1)
N:Alternate names: delta-endotoxin IC1; entomocidal crystal protein
C:Species: Bacillus thuringiensis
A:Variety: strain aizawai IC1
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S02134; S04994
R:Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A:Title: Nucleotide sequence of a Bacillus thuringiensis aizawai IC1 entomocidal crystal protein
A:Reference number: S02134; MUID:89083518; PMID:3205732
A:Accession: S02134
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1155 <HAI>
A:Cross-references: UNIPROT:P06578; EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A:Experimental source: strain aizawai IC1
R:Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes in the C-terminal region of the delta-endotoxin of Bacillus thuringiensis strain aizawai IC1
A:Reference number: S04994; MUID:89362455; PMID:2769751
A:Accession: S04994
A:Molecule type: DNA
A:Residues: 429-449, 'A', 451-724 <HAW>
A:Cross-references: EMBL:X16315
A:Experimental source: strain aizawai IC1
C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 26.6%; Score 906.5; DB 2; Length 1155;
Best Local Similarity 33.5%; Pred. No. 6.7e-50;
Matches 221; Conservative 120; Mismatches 228; Indels 91; Gaps 24;
Qy 31 DPNSTLEELNYKEFLRMTESSSTEVLDSSTVKDVGTVGISVVG-----QILGVGVGVP 84
Db 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE-----TGYPIDISLSITQFLSEFVG 53
Qy 85 AGALTSFYQSFLNTIWI---PSDADPWKAFMAQVEVLIDKKIEYAKSKALAEQLQNN 140
Db 54 AG----FVLGLVDIWIIGIFGPSQ---WDAFLVQIEQLINQRIEFPARNQAISSLGLSNL 106
Qy 141 FEDYVNLNWKKTPLSLRSKRSQDRIRELFQSAESHFNSMPSFAVSKFELVLPYVQ 200
Db 107 YQIVAESFWEADPTN-PALREMRIQ--FNDMNSALTUATPLFAVQNYQVPLLSVVVQ 163
Qy 201 AANTHLLLLKDAQVFGREWGYSSEDAEFYHRQLKLTQQYTDHCVNWNVYVGLNGRSTY 260
Db 164 AANLHLSVLRDVSFVQGRWGFDAARINSRYNDLTRIGNYTDHAVRWYNTGLRWGPD 223
Qy 261 DAWKFNFRREMTLVLDLIVLPFFYDRIYLSKGVKTELTDRIDTPIPSLNTLOEYGP 320
Db 224 RDWIRYNQFRREMTLVLDLIVLSLFPNYSRTYPIRTVSQLTREIYTNPV-----LENFDG 278

C:Genetics:

A:Gene: cry-1-2; bt2
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin
F:82-586/Product: toxic peptide #status predicted <TXP>
F:82-300/Region: toxic #status predicted
F:300-586/Region: insecticidal #status predicted

Query Match 26.4%; Score 899.5; DB 2; Length 1155;
Best Local Similarity 33.3%; Pred. No. 1.9e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

QY 31 DNPNSLEELNYKEFLRMTESSSTVLDNSTVKDVGTSISVVG-----QILGVVGVPP 84
DB 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYTPIDISLSLTQFLSEFPVG 53
QY 85 AGALTSFYQSFLNTIW-----PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNN 140
DB 54 AG-----FVLGLVDIILWIGIFGPSQ---WDAFLVQIQLINQRIEFAFNQAIISRLGLSNL 106
QY 141 FEDYVNALNWKKTPLSLRSKRSQDRIRLEFSAESHFNFSMPSPFAVSKFEVFLFPTYQA 200
DB 107 YQIYAESFREWADPTN--PALREEMRIQ--FNDMNSALTATTAIPLEAVQNYQVPLLSTVYVQ 163
QY 201 AANTHLLLLKDAQVFGEEWYSSDVAEFYHRQLKLTQOYTDHCYNNVYVGLNGLRGSTY 260
DB 164 AANLHLSVLRDVSFQGRWGFDAAATINSRYNDLTRIGNYTDHAVRWYNTGLERVMGPD 223
QY 261 DAWVKENRRREMTLTVDLIVLPFYDRLYKGVKTELTRDIFTDPIFSLNTLQEQYCP 320
DB 224 RDMIRYNQFRRELTLVDIVSLFNPYDSRTPIRVTSQLTREIYNPV-----LENFDG 278
QY 321 TP-----LSIENSIRKPHLDYLGIEFHTRLQPGYFGKDSFNWGSYNYVETRPISGSKT 376
DB 279 SFRGSAQIEGSIKSPHMLDILNSITITDARGEY-----YWSGHQIMASPVGSPGE 332
QY 377 ITSPPFYGDK-STEPVQKLSFD-COKYVRIANTDVAAMPNGKVY-----LGVTKVDFSQY 429
DB 333 FTPEPLYGTMGNAAPQORIVAQLQGQVYRTLSST-----LYRRPFNIGINNQLSVL 383
QY 430 DDQKNETSTQT-----YDSKRNGHVSAQDSIDQLPETTDEPLEKAYSHQINYAECFL 483
DB 384 DGTFFAYGTSNLPASVY---RKSQTV---DSLDEIPQNNVPPRQGFSHRLSHVSMFR 437
QY 484 MQDRRGTI-----PFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGFTG 538
DB 438 SGFSNSSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGFTG 497
QY 539 NLLFLKSSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQ-----NSNNDFLVI 592
DB 498 DIL-RTSPQGI STLVRNI--TAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGN-----550
QY 593 YINKTMNKDDDLTYQTFDLATTNMFGSKDKNELIIGAESFVSNKEIYIDKIEPIPVQL 652
DB 551 -FSATMSSGSLQSGSPRTVGTFTPFNFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609

RESULT 20

A29125
parasporal crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29125
R:Fishchoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederm
Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.
A:Reference number: A29125
A:Accession: A29125
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPROT:Q93721
C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 26.4%; Score 899.5; DB 2; Length 1156;
Best Local Similarity 33.3%; Pred. No. 1.9e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

QY 31 DNPNSLEELNYKEFLRMTESSSTVLDNSTVKDVGTSISVVG-----QILGVVGVPP 84
DB 3 NNPIN-ECIPY-----NCLSNPEVEVLGGERIE---TGYTPIDISLSLTQFLSEFPVG 53
QY 85 AGALTSFYQSFLNTIW-----PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNN 140
DB 54 AG-----FVLGLVDIILWIGIFGPSQ---WDAFLVQIQLINQRIEFAFNQAIISRLGLSNL 106
QY 141 FEDYVNALNWKKTPLSLRSKRSQDRIRLEFSAESHFNFSMPSPFAVSKFEVFLFPTYQA 200
DB 107 YQIYAESFREWADPTN--PALREEMRIQ--FNDMNSALTATTAIPLEAVQNYQVPLLSTVYVQ 163
QY 201 AANTHLLLLKDAQVFGEEWYSSDVAEFYHRQLKLTQOYTDHCYNNVYVGLNGLRGSTY 260
DB 164 AANLHLSVLRDVSFQGRWGFDAAATINSRYNDLTRIGNYTDHAVRWYNTGLERVMGPD 223
QY 261 DAWVKENRRREMTLTVDLIVLPFYDRLYKGVKTELTRDIFTDPIFSLNTLQEQYCP 320
DB 224 RDMIRYNQFRRELTLVDIVSLFNPYDSRTPIRVTSQLTREIYNPV-----LENFDG 278
QY 321 TP-----LSIENSIRKPHLDYLGIEFHTRLQPGYFGKDSFNWGSYNYVETRPISGSKT 376
DB 279 SFRGSAQIEGSIKSPHMLDILNSITITDARGEY-----YWSGHQIMASPVGSPGE 332
QY 377 ITSPPFYGDK-STEPVQKLSFD-COKYVRIANTDVAAMPNGKVY-----LGVTKVDFSQY 429
DB 333 FTPEPLYGTMGNAAPQORIVAQLQGQVYRTLSST-----LYRRPFNIGINNQLSVL 383
QY 430 DDQKNETSTQT-----YDSKRNGHVSAQDSIDQLPETTDEPLEKAYSHQINYAECFL 483
DB 384 DGTFFAYGTSNLPASVY---RKSQTV---DSLDEIPQNNVPPRQGFSHRLSHVSMFR 437
QY 484 MQDRRGTI-----PFFTWTHRSVDFNTDAEKITQLPVVKAYALSSGASIIIEGPGFTG 538
DB 438 SGFSNSSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPLTKSTNLGSGTSVVKPGFTG 497
QY 539 NLLFLKSSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQ-----NSNNDFLVI 592
DB 498 DIL-RTSPQGI STLVRNI--TAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGN-----550
QY 593 YINKTMNKDDDLTYQTFDLATTNMFGSKDKNELIIGAESFVSNKEIYIDKIEPIPVQL 652
DB 551 -FSATMSSGSLQSGSPRTVGTFTPFNFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 609

RESULT 21

A42459
parasporal crystal protein cryIaF - Bacillus thuringiensis (strain aizawai)
N:Alternate names: parasporal crystal protein cryIaF
C:Species: Bacillus thuringiensis
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene from
C:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: A42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <CHA>
A:Cross-references: UNIPROT:Q03746; GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 26.4%; Score 898.5; DB 2; Length 1174;
Best Local Similarity 34.5%; Pred. No. 2.2e-49;
Matches 204; Conservative 104; Mismatches 221; Indels 63; Gaps 14;

QY 82 VPPAGALTSFYQSFLNTWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNNF 141
DB 49 VPGVGAFGLPDLIWLWGFIITSD---NSLFLQLIQLEQRIETLERNRAITTLRGLADSY 105
QY 142 EDYVNALNSKKTPLSLRKSRQDRIRBELFSQAESHFRNSMPSFAVSKFVFLPPTYAQA 201
DB 106 EIVTEALREWEANP---NNAQLREDVRIRFANTDDALITAINFTLTSFPIPLSVVQA 162
QY 202 ANTHLLLLKDAQVGEWGYSSSEDVAEFYHRQLKLTQOYTDHCNVNWNVGLNGLRSTYD 261
DB 163 ANLHLSLRDAVFGQWGLDIAIVNNHYNRLNLHRYTKGLCLDTYNOGLENLRGNTNR 222
QY 262 AMVKFNFRREMTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOEYGP 321
DB 223 QWAFNQFRDLTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOEYGP 282
QY 322 -FUSIENSIRKPHLDYLOQIEBHT-----RLQPGYFGKDSFNWYSGNMYVETRSIGSSKT 376
DB 283 GFNRAEFGVRPPLMDPMNSL-FVTAETVRSQ-----TWGGLVSSRNAGN--R 330
QY 377 ITSPPFYG-----DKSTEPVQKLSFDGQKVYRTIANTDV--AAWPNKVKYLGVTX 423
DB 331 INFPSYGVFNPGGAIWADSDPRP-----FYRTLSDPVFRVCGFNPHYVLGLRG 380
QY 424 VDFSQYDDQKNETSTQFYDSKRNNGHVSAODSIDQLPPETTDDEPLEKAYSHQNLNABCF- 482
DB 381 VAQQ-----TGTNHTRTFRNSGTI---DSLDEIPQDNSGAPWMDYSHVLNHTFVR 430
QY 483 -----LMODRRGTIPFPFWTHRSVDFNTIDAETKITQLPVVKAYALSSGASIIIEGPGFTGG 538
DB 431 WPGEISGDSWRAPMFESWTHRSATPTNTIDPERITQIPLVKAHTLQSGTTVVRGPGFTGG 490
QY 539 NLLFLKSSNSIAKFKVTLNSALLQRYRIRYASTNLRFLVQNSNNDPLVIYINKTM 598
DB 491 DI--LRTSGGPFAYTIVNQLPQRYRIRYASTNLRIRYTVVAGERIFAPQGFNKTW 548
QY 599 NKDDDLTYQTFDLATNNSNGFSGDKNELIIGAESFVSNKEIYIDKIEPIPV 650
DB 549 DTGDPITFQSFVATINTATTFPMSSQSFVVGADTFSSGNEVIDRPELIPV 600

RESULT 22
I39838
paraesporal crystal protein - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39838
J;Hefford, M.A.; Brousseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.
J;Biotechnol. 6, 307-322, 1987
A;Title: Sequence of a lepidopteran toxin gene of Bacillus thuringiensis subsp kurstaki
A;Reference number: I39838
A;Accession: I39838
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1155 <RES>
A;Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA22420.1; PID:g142886
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 26.3%; Score 895.5; DB 2; Length 1155;
Best Local Similarity 33.3%; Pred. No. 3.4e-49;
Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

QY 31 DNPNSTLEENLYKEFLRMTSDSTEVLDNSTVKDVGCTGISVVG-----QILGVGVGVFP 84
DB 3 NNPNIN-ECIPY-----NCLSNPEVLGGERIE---TGYPIDISLSLTQFLLSFVPG 53
QY 85 AGALTSFYQSFLNTW---PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQNN 140
DB 54 AG-----FVLGLDIIWIGIFPSQ---WDAFLVQIEQLINQRIEIEFARNQAIISRLGSLN 106
QY 141 FEDYVNALNSKKTPLSLRKSRQDRIRBELFSQAESHFRNSMPSFAVSKFVFLPPTYAQ 200

DB 107 YQIYAESFREWEADPTN-PALREEMRIQ---ENDMNSALTTTAAIPLFAVQNVQVPLSVVQ 163
QY 201 ANTHLLLLKDAQVGEWGYSSSEDVAEFYHRQLKLTQOYTDHCNVNWNVGLNGLRSTY 260
DB 164 ANLHLSLRDAVFGQWGFDAATINSRYNDLTIRLIGNYTDHAVRWYNTGLERWGPDS 223
QY 261 DAMVKFNFRREMTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOEYGP 320
DB 224 RDMIRYNQFRELTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOEYGP 278
QY 321 TP-----LSIENSIRKPHLDYLOQIEBHTLQPGYFGKDSFNWYSGNMYVETRSIGSSKT 376
DB 279 SPRGSAQIEGSIKSPHMLDINSITITTDARGEY-----YWSGHQIIMASPVGFSQPE 332
QY 377 ITSPPFYGDK-STEPVQKLSFD-CQKVYRTIANTDVAAWPNKQY-----LGVTKVDFSOY 429
DB 333 FTFPLTYGTMGNAAPQORIQAQGGQVYRTLSST-----LYRRPFNTGINNQQLSVL 383
QY 430 DDOKNETSTOT-----YDSKRNNGHVSAODSIDQLPPETTDDEPLEKAYSHQNLNABCF 483
DB 384 DGTPEYAGTSSNLPASVY---RKSGTV---DSLDEIPQDNNVPPROGFRHRLSHVSMFR 437
QY 484 MODRRGTI-----PFTWTHRSVDFNTIDAETKITQLPVVKAYALSSGASIIIEGPGFTGG 538
DB 438 SGFSNSSVSIIRAPMFESWTHRSANFNIIIPSSQITQIPLTKSTNLGSGTSVVRGPGFTGG 497
QY 539 NLLFLKSSNSIAKFKVTLNSALLQRYRIRYASTNLRFLVQNSNNDPLVIYINKTM 592
DB 498 DIL-RRTSPQISTLRVNI-TAPLSQRYRIRYASTNLRFLVQNSNNDPLVIYINKTM 550
QY 593 YINKTNKDDDLTYQTFDLATNNSNGFSGDKNELIIGAESFVSNKEIYIDKIEPIPV 652
DB 551 -PSATWSSGNSLQSGFRHLGFTTPFNFSNGSSVFLSAHVFNCSGNEVYIDRIEFVPAEV 609

RESULT 23
A41052
paraesporal crystal protein cryAel - Bacillus thuringiensis (strain aleati)
C;Species: Bacillus thuringiensis
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41052
J;Lee, C.S.; Aronson, A.I.
J;Bacteriol. 173, 6635-6638, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subsp
A;Reference number: A41052; MUID:92011442; PMID:1655719
A;Accession: A41052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1181 <LEE>
A;Cross-references: UNIPROT:Q03748; GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
C;Superfamily: paraesporal crystal protein
C;Keywords: delta-endotoxin

Query Match 26.1%; Score 888; DB 2; Length 1181;
Best Local Similarity 34.6%; Pred. No. 1.1e-48;
Matches 206; Conservative 107; Mismatches 222; Indels 60; Gaps 18;

QY 82 VPPAGALTSFYQSFLNTW---PSDADPWKAFMAQVEVLIDKKIEEYAKSKALAEQLQ 137
DB 51 VPGAG---FVLGLDIIWIGFVPSQ---WDAFLVQIEQLISQRIEIEFARNQAIISRL 103
QY 138 QNNFEDYVNALNSKKTPLSLRKSRQDRIRBELFSQAESHFRNSMPSFAVSKFVFLP 197
DB 104 SNYQIYIAEAFREWEADPTN-PALREEMRIQ---FNDMNSALTTTAAIPLFTVQNVPLSV 160
QY 198 YQAQANTHLLLLKDAQVGEWGYSSSEDVAEFYHRQLKLTQOYTDHCNVNWNVGLNGLRG 257
DB 161 YQAVNLHLSVLRDVSFVGQWGLDVATINSRYNDLTIRLIGNYTDHAVRWYNTGLERW 220
QY 258 STYDAMVKFNFRREMTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOE 317
DB 221 PDSRDWRYNQFRELTLTVLDLIVLPFPFYDIRLSYKGVKTELTRDFTDPIFSLNTLOE 275

[illegible]

411 AMPNGKYL-GVTKVDFSOYDDOKNETSTQTYDSKRNGHVSAQDSIDQLPPETTDPELE 469
375 PWPAPPENLRGVEGVFS-----TPIINSPTY---RGRGTV---DSLTELPEPDSVPPR 422
470 KAYSHQINVAECFLMQDRGTI-----PFTWTHRSVDFFENTIDAEKITQLPVVKAYALS 524
423 EGYSHRLCHA---TFVQRSGTPTLTGPFVFSWTHRSATDRNIIPYDVINQIPLVKAFNLT 479
525 SGASIIETGPGFTGNNLILFLKESNSIAKFKVTLN-SAALQRYRVRIRYASTTNLRLFY- 582
480 SGISVVRGPGFTGGDIIRTVNGSVLS---MSLNFSNTTLQRYRVRVRYAASQTMVMSVT 536
583 -----QNSNNDPLVIYINKTWKDDLLIYQFDLATTNSMGFGSKNELIIGAESFVN- 637
537 VGGSTTCNQGF-----PSTMSANGALTSQSFRFAFPVGISASGSQ-----GASISISNN 586
638 ---EKIYIDKIEFIPV 650
587 VGRQMFHLDRIEFLPV 602

RESULT 25
JT0241
Parasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)
N:Alternate names: 135k insecticidal protein
C:Species: *Bacillus thuringiensis*
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JT0241
R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A:Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein
A:Reference number: JT0241
A:Accession: JT0241
A:Molecule type: DNA
A:Residues: 1-1176 <SH1>
A:Cross-references: UNIPROT:P02965
A:Note: b. thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal proteins
C:Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 25.7%; Score 876; DB 2; Length 1176;
Best Local Similarity 32.9%; Pred. No. 6.2e-48;
Matches 215; Conservative 120; Mismatches 240; Indels 78; Gaps 22;

QY 31 DNPNTSLBELNYKEFLRMETDSSTVELDNSTVKDAVGTGTSVVG-----QILGVVGVFP 84
DB 3 NNPIN-ECIPY----NCLSNPEVEVLGGERIE-----TGYPIDISLSLTQFLSEFPVG 53
QY 85 AGALTSFYQSFLNTIW----PSDADPWKAFMAQVEVLIDKKIEBYAKSKALAELOGLQNN 140
DB 54 AG-----FVLGLVDIWGIFGPSQ---WDAFLVQIEQLINQRIEESFARNQAIISRLGSLN 106
QY 141 FEDYVNALNSKKITPISLRKRSQDRRELFSQAESHFNRSPSFVSKFEVLFLPTVAQ 200
DB 107 YQIYAESFREWEADPTN-PAIREEMRIQ--FNDMNSALTTPAIPFAVQNYQVPLLSVYVQ 163
QY 201 AANTHILLKDAQVFGREWGYSDDAEFYHRQLKLTQYTDHCVNWNVNLGLNRGSTY 260
DB 164 AANLHLSVLSDVSFGQWGFDAATINSRYNDLTRIGNYTDYAVRWYNTTGLERVWGPDS 223
QY 261 DAWVKPFRREMRTLTVLDDLIVLFFPDYRLXSGVKTELTRDIFDPSLNTIQEVGP 320
DB 224 RDWRYNQFRELTLTVLDIVALFSNYSRRYPRTVSQLTRFIYTNPV-----LENFDG 278
QY 321 TELS-----IENSIRKPHLFDYLOGIEFHTRLQPGYFGKDSFNWYSGNVVETSPSGSKT 376
DB 279 SFRGMAQRLEQNIQPHLMDILNSTIIVTDVHRG-----FNWYSGHQITASPGVSGPGE 332
QY 377 ITSFPYGDK-STEPVQKLSFPQKQVRYTIAN-----TDVAAMPNGKYLGVTKVDFSOYD 430
DB 333 FAFLFLGNAGNAAPPVLVSLTGLGFIIRUSSPFLRIILGSGPNQNELFVLDDGTESFAS 392

QY 431 DQKNETSTQYDSKRNGHVSADSIDQLPETTDEPLEKAYSHOLNVAECFLMDDRGT 490
Db 393 LTTNLST-----IYRQGTG---DSDLVIPPQNSVPPRAGFHRLSHVT--MLSAQA 443
QY 491 I-----PFFTWTTHRSVDFNTIDAETITQLPVVKAYALSSGASIIIEGPGFTGNNLLFLKE 545
Db 444 VYTLRAPTFWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDIL--RRT 502
QY 546 SSSNSIAKFKVTLNSAALLQRYVRIRYASTNLRFLVQ-----NSNDFLVIYINKTMN 599
Db 503 SPOQISTLRVNI--TAPLSQRYVRIRYASTTNLFQHTSIDGRPINQGN-----FSATMS 555
QY 600 KDDDLTYQTFLATTNSMGFGDKNELIIGAESFVSNKIIYIDKIEFIPVOL 652
Db 556 SGNLSQSGSRFTVGTPTPFNFSGSVFTLSAHVFNSGNEVIYIDRIEFVPAEV 608
RESULT 26
A22798
paraasporal crystal protein - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C:Accession: A22798
R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Izuka, T.; Sugisaki, M.; Takanami, M.
Gene 34, 243-251, 1985
A:Title: Nucleotide sequence coding for the insecticidal fragment of the Bacillus thuringiensis
A:Reference number: A22798; MUID:85232070; PMID:2989108
A:Accession: A22798
A:Molecule type: DNA
A:Residues: 1-934 <SH1>
A:Cross-references: UNIPROT:Q9SSV8; GB:M10917; NID:g143100; PIDN:AAA22552.1; PID:g551713
A:Comment: The authors translated the codon ACA for residue 264 as Ser.
C:Superfamily: paraasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 25.7%; Score 874; DB 2; Length 934;
Best Local Similarity 32.9%; Pred. No. 5.9e-48;
Matches 215; Conservative 120; Mismatches 240; Indels 78; Gaps 22;
QY 31 DNPNSTLEELNYKEFLRMTEDESSTVEDNSTVKDVGTSVVG-----QILGVGVGVPF 84
Db 3 NNPEN-ECIPY-----NCLSNPEVEVLGGERIE---TGYPIDISLSLTQFLSSEVPFG 53
QY 85 AGALTSFYQSFLNTIW-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQNN 140
Db 54 AG-----FVLGLVDIIIGIFGPSQ---WDAPLVIQELINRIIEFARNQAIISRLGSLN 106
QY 141 FEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLPLPTAQ 200
Db 107 YQIYAESFREWADPTN--PALREMRIQ--FNDMNSALITTAIPLFAVQNVQVPLLSVYVQ 163
QY 201 AANTHLLLLKDAQVGEWGYSSDVAEFYHRLQKLTQQYTDHCVNWNVGLNGLRGSTY 260
Db 164 AANLHLVLRLDVSFVGQWGFDAATNSRYNDLTRIGNYTDYAVRWYNTGLERVMGSDS 223
QY 261 DAWVKENRREREMTLVLDLIVLPFYDRLYSKGVKTELTDIFDTPFSLNTLOEYGP 320
Db 224 RDWRVYNQFRRELTVLVDIVLFSYDSRRYPIRTVSQLTREIYTNPV-----LENFDG 278
QY 321 TFLS-----IENSIRKPHLEFDYLOGIEFHTLRLOPGYFGKDSFNWWSGNYVETRESIGSKT 376
Db 279 SFRGMAQRIEQNIQPHLMILNRIITYTDVHRG-----FNWWSGHQITASVPFGSGPE 332
QY 377 ITSPPFYGDK-STEPVOKLSFDGQKVYRTIAN-----TDVAAMPNGKVYLGVTGVKDFVSQYD 430
Db 333 FAPFLFGNAGNAAPPVLVSLTGLIGFRTLSPLRYRIILGSGNNQELFVLDGTEFSFAS 392
QY 431 DQKNETSTQYDSKRNGHVSADSIDQLPETTDEPLEKAYSHOLNVAECFLMDDRGT 490
Db 393 LTTNLST-----IYRQGTG---DSDLVIPPQNSVPPRAGFHRLSHVT--MLSAQA 443
QY 491 I-----PFFTWTTHRSVDFNTIDAETITQLPVVKAYALSSGASIIIEGPGFTGNNLLFLKE 545
Db 503 SPOQISTLRVNI--TAPLSQRYVRIRYASTTNLFQHTSIDGRPINQGN-----FSATMS 555
QY 600 KDDDLTYQTFLATTNSMGFGDKNELIIGAESFVSNKIIYIDKIEFIPVOL 652
Db 556 SGNLSQSGSRFTVGTPTPFNFSGSVFTLSAHVFNSGNEVIYIDRIEFVPAEV 608

Db 444 VYTLRAPTFWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDIL--RRT 502
QY 546 SSSNSIAKFKVTLNSAALLQRYVRIRYASTNLRFLVQ-----NSNDFLVIYINKTMN 599
Db 503 SPOQISTLRVNI--TAPLSQRYVRIRYASTTNLFQHTSIDGRPINQGN-----FSATMS 555
QY 600 KDDDLTYQTFLATTNSMGFGDKNELIIGAESFVSNKIIYIDKIEFIPVOL 652
Db 556 SGNLSQSGSRFTVGTPTPFNFSGSVFTLSAHVFNSGNEVIYIDRIEFVPAEV 608
RESULT 27
JC2219
paraasporal crystal protein cryIaA - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Bioeci. Biotechnol. Biochem. 58, 830-835, 1994
A:Title: Cloning of a new cryIA(a) gene from Bacillus thuringiensis strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972
A:Accession: JC2219
A:Molecule type: DNA
A:Residues: 1-1176 <UDA>
A:Cross-references: UNIPROT:Q45736; DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g5357
A:Gene: cryIA(a)
A:Superfamily: paraasporal crystal protein
C:Keywords: delta-endotoxin
Query Match 25.5%; Score 870; DB 2; Length 1176;
Best Local Similarity 32.8%; Pred. No. 1.5e-47;
Matches 214; Conservative 120; Mismatches 241; Indels 78; Gaps 22;
QY 31 DNPNSTLEELNYKEFLRMTEDESSTVEDNSTVKDVGTSVVG-----QILGVGVGVPF 84
Db 3 NNPEN-ECIPY-----NCLSNPEVEVLGGERIE---TGYPIDISLSLTQFLSSEVPFG 53
QY 85 AGALTSFYQSFLNTIW-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQNN 140
Db 54 AG-----FVLGLVDIIIGIFGPSQ---WDAPLVIQELINRIIEFARNQAIISRLGSLN 106
QY 141 FEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLPLPTAQ 200
Db 107 YQIYAESFREWADPTN--PALREMRIQ--FNDMNSALITTAIPLFAVQNVQVPLLSVYVQ 163
QY 201 AANTHLLLLKDAQVGEWGYSSDVAEFYHRLQKLTQQYTDHCVNWNVGLNGLRGSTY 260
Db 164 AANLHLVLRLDVSFVGQWGFDAATNSRYNDLTRIGNYTDYAVRWYNTGLERVMGSDS 223
QY 261 DAWVKENRREREMTLVLDLIVLPFYDRLYSKGVKTELTDIFDTPFSLNTLOEYGP 320
Db 224 RDWRVYNQFRRELTVLVDIVLFSYDSRRYPIRTVSQLTREIYTNPV-----LENFDG 278
QY 321 TFLS-----IENSIRKPHLEFDYLOGIEFHTLRLOPGYFGKDSFNWWSGNYVETRESIGSKT 376
Db 279 SFRGMAQRIEQNIQPHLMILNRIITYTDVHRG-----FNWWSGHQITASVPFGSGPE 332
QY 377 ITSPPFYGDK-STEPVOKLSFDGQKVYRTIAN-----TDVAAMPNGKVYLGVTGVKDFVSQYD 430
Db 333 FAPFLFGNAGNAAPPVLVSLTGLIGFRTLSPLRYRIILGSGNNQELFVLDGTEFSFAS 392
QY 431 DQKNETSTQYDSKRNGHVSADSIDQLPETTDEPLEKAYSHOLNVAECFLMDDRGT 490
Db 393 LTTNLST-----IYRQGTG---DSDLVIPPQNSVPPRAGFHRLSHVT--MLSAQA 443
QY 491 I-----PFFTWTTHRSVDFNTIDAETITQLPVVKAYALSSGASIIIEGPGFTGNNLLFLKE 545
Db 444 VYTLRAPTFWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPFTGGDIL--RRT 502
QY 546 SSSNSIAKFKVTLNSAALLQRYVRIRYASTNLRFLVQ-----NSNDFLVIYINKTMN 599

Db 503 SPGQISTLRVNI-TAPLSQRYRVRIRYASTVNTLQFHTSIDGRPINQGN-----FSATMS 555

Qy 600 KDDDLTYQTDLATNSNMFGSGDKNELIIGAESFVSNEKIYIDKIEFIPVOL 652

Db 556 SGNLQSGSPTVGTFTTFNFNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV 608

RESULT 28

I40572

Parasporal crystal protein cryICb - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C:Accession: I40572

R:Boesse, M.; Masson, L.; Brousseau, R.

Nucleic Acids Res. 18, 7443, 1990

A:Title: Nucleotide sequence of a novel crystal protein gene isolated from Bacillus thuringiensis

A:Reference number: I40572; MUID:91081338; PMID:2259636

A:Accession: I40572

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1171 <RES>

A:Cross-references: UNIPROT:Q57458; EMBL:X56144; NID:g40281; PIDN:CAA39609.1; PID:g40282

C:Genetics:

A:Gene: cryIC(b)

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 25.5%; Score 869.5; DB 2; Length 1171;
Best Local Similarity 33.7%; Pred. No. 1.6e-47;
Matches 219; Conservative 117; Mismatches 241; Indels 73; Gaps 21;

Qy 19 ELQTNHQ---YPLADPNSTLELNKYEFRLMTWEDSTVELDNSTVKDVGTCISVVGQ 75

Db 2 EIVANNQCVFNYCLNPN-----EILDIERNSTVATNIALEIS 42

Qy 76 ILGVGVVPFAGALTSFYOSFLNTIWPSDADPWKAFMAQVEVLIDKIEEYAKSKALAEQ 135

Db 43 RLLASATPIGILGLFDPAIWGSIQPSQ---WDLFLEQIELLIDQKIEFARNQAISRL 99

Qy 136 GLQNNFEDYNALMSWKTPLSLRKSQSDRIRELFSQAESHFNPSFAVSKFEVLEL 195

Db 100 GISSLYGIYTEAFREWEADPTNPALK---EEMRTQFNDMNSILVTALPLFSVQNYQVPEL 156

Qy 196 PTYQAANTHLLLKDAQVFGEEGYSSDVAEPVHRQKLTOQYDHCVMVNVVGLN-- 253

Db 157 SVYVQAAMHLHSLVLDVSVFGQMGFDIATNSRYNDLTRLIPIYTDVAVRYNTGLDRL 216

Qy 254 ---GLRGSTYDAWVKFNRFRMTLTLDLIVLPFPYDILYKSGVKVTELTDRIDTPI 309

Db 217 PRTGGLRN-----WARFNQFRELITISVLDIISFPNVDLSRLYPIPTSSQUTREVYTDV 271

Qy 310 PSLNTLQBYGPTFLSIENS-IRKPHLPDYLOQIEPHTRLQPGYFGKDSFNYSWNGVYETR 368

Db 272 INI-TDYRVGSPFENIENSIRSPHLMDFLNLITDIDLIRG-----VHYWAGHRV-TS 323

Qy 369 PSIGSKKTIISPFYG-DKSTEP---VQKLSFDGQKV-YRTIANTDVAAPNGKYVLGVTK 423

Db 324 HFTGSSQVITTPQYGITANAEPRTIAPTFTPLGLNLFYRTLSPNPFRRSENIITPLGINV 383

Qy 424 VDFSQDDQKNETSTQTVDKRNNGHVAQSDIDOLPETTDEPLEKAYSHOLNAVEC-- 481

Db 384 VQGVGFIQPNN--AEVLY---RSRGTV---DSLNEPLIDGENSLV--GYSHRLSHVILTR 433

Qy 482 FLMQDRRGITPFTWTHRSVDPFNTIDAEKITQLPFWKAYALSSGASIEGFGTGNLL 541

Db 434 SLVYNTNITSLPFWVTHSATNTNINPDITQIPLVKGFRLLGGTSVKGFGTGGDIL 493

Qy 542 FLKESNSIAKF---KVLNSAALLQYRVRIYASTVNTLRLFVQNSNDPLFVIYINKTM 598

Db 494 ----RRNTIGEVSQVNVINS-PITQYRLRFPYASSRDARITVAIGQIRVDMTLEKTM 548

Qy 599 NKDDDLTYQTDLATNSNMFGSGDKNELIIGAESFVSNEKIYIDKIEFI 648

Db 549 EIGESLTSRTFSYTNFNSFPFRANPDIIIRIABELPIRGGLYIDKIELI 598

RESULT 29

A37829

parasporal crystal protein cryIEal - Bacillus thuringiensis

C:Species: Bacillus thuringiensis

C:date: 14-Jun-1991 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: A37829; S13762; S14438

R:Visser, B.; Munsterman, E.; Stoker, A.; Dirkse, W.G.

J. Bacteriol. 172, 6783-6788, 1990

A:title: A novel Bacillus thuringiensis gene encoding a Spodoptera exigua-specific crystal protein

A:reference number: A37829; MUID:91072224; PMID:2254254

A:Accession: A37829

A:Molecule type: DNA

A:Residues: 1-1171 <VI2>

A:Cross-references: UNIPROT:O06894; EMBL:X53985

A:Note: translation is incomplete

C:Superfamily: parasporal crystal protein

C:keywords: delta-endotoxin

Query Match 25.5%; Score 869.5; DB 2; Length 1171;

Best Local Similarity 33.7%; Pred. No. 1.6e-47;

Matches 219; Conservative 117; Mismatches 241; Indels 73; Gaps 21;

Qy 19 ELQTNHQ--YPLADNPSTLEELNYKEFLRMTESSSTEVLNDNSTVKDAVGTSIVVGQ 75

Db 2 EIVNNQCVPCYNLNPEN-----EILDIERNSVATNIALEIS 42

Qy 76 ILGVGVVPPFAGALTSFYQSFLNTIWPSDADPKWPAQVEVLIDKKIEYAKSKALAEIQ 135

Db 43 RLLASATPIGGILLGLFDALWGSIGFSQ---WDLFLEQIELLIDQKIEFARNQAISRL 99

Qy 136 GLQNNFEDYNALNSWKKTPLSLRSKRSODRLRELFSQAESHFRNSMPPSPFAVKFVLFL 195

Db 100 GISLLYGLYTEAFREWEADPTNPALK---EENRTQFENDMNSILVTAIPLESVQNYQVFL 156

Qy 196 PTYQAQANTHLLKDAQVGEWGYSSSDVAEFYHRQLKLTQQYTDCHCVNWNVGLN-- 253

Db 157 SVVYQAAANLHLSVLKDVSVFGQAWGFDIATINSRYNDLTRLPIDYDVAVRWNTGLDRL 216

Qy 254 ---GLRGSTDYDAWKFNFRREMTLVLDLVLPPFYDIRLYSKGVKTELTRDIFTDPI 309

Db 217 PRTGGLRN---WARFNQFRRELTISVLDDIISFFPNYDSRLPIPTSSQLTREYVTDPV 271

Qy 310 FSLNTLQYGGTFTLSIENS-IRKPHLFDYLOGIEFHTRLQPGYFGKDSFNWGSNNYVETR 368

Db 272 INI-TDYRVGSFENIENSAIRSPHMLDFNLNLTIDTLIRG-----VHYWAGHRV-TS 323

Qy 369 PSIGSKTITSPFYG-DKSTEP---VQKLSFGQKV-YRTIANTDVAAWNGKVLGVTK 423

Db 324 HFTGSQVITTPQYGITANAEPRTIAPTPTFGLNLFYFRTLSNPPFRFRSNIPTTLGLNV 383

Qy 424 VDFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPTTDEPLEKAYSHQLNAYEC-- 481

Db 384 VQGVGFQPNV--AEVLY---RSRGTV---DSLNELPIDGENSLV--GYSHRLSHVLTIR 433

Qy 482 FLMDRRGTIPFTWTHRSVDFTNTIDASKITQLPVVKAYALSSGASIIIGPGTGGNLL 541

Db 434 SLYNTNITSLPTFVWTHHSATNTNTINPDIITQIPLVKGFRLGGGTSVIKPGPGTGDIL 493

Qy 542 FLKSSNSITAKP---KVTLSAALLQRYVRIRYASTTNLRLLFVQNSNNDPLVYINKMT 598

Db 494 ---RRNTIGEFVSIQVNNIS-PITQRYLRIRFYASRDARIITVAIGQIRVDMTLEKTM 548

Qy 599 NKDDLTLYQTFLATNTSNMGFGDKNEIIGAESFVNSKEKIYIDKIEFI 648

Db 549 EIGESLTSRTFSYTNFNSFPFRANPDIIIRIABELPIRGGLYIDKIELI 598

RESULT 30

A49785

parasporal crystal protein cryIA(c) - Bacillus thuringiensis subsp. kenya (strain HD568)

C;Species: Bacillus thuringiensis subsp. kenya
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A49785
R;Von Tersch, M.A.; Robbins, H.L.; Jany, C.S.; Johnson, T.B.
Appl. Environ. Microbiol. 57, 349-358, 1991
A;Title: Insecticidal toxins from Bacillus thuringiensis subsp. kenya: gene cloning and
A;Reference number: A49785; MUID:91197102; PMID:2014985
A;Accession: A49785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1177 <VON>
A;Cross-references: UNIPROT:Q45735; GB:M35524; NID:g142739; PIDN:AAA22338.1; PID:g142740
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 25.5%; Score 867.5; DB 2; Length 1177;
Best Local Similarity 33.7%; Pred.No.2.2e-47;
Matches 220; Conservative 110; Mismatches 242; Indels 81; Gaps 24;

```
QY 31 DNPNSTLEELNYKEFLRMTESSTEVLNDNSTVDAVGTGISVVG-----QILGWVGVPF 84
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 3 NNPEN-ECIPY----NCLSNPEVEVLGGERIE----TGYTPIDISLSLTQFLSEFVPG 53

QY 85 AGALTSYQSFNTIWM-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQGN 140
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 54 AG----FVLGLVDIIMGIFGPSQ---WDAFLVQIEQLINQRIEFARNAQISRLEGLSNL 106

QY 141 FEDYVNALNSWKKTPLSLRSKRQDRIRLEFSQAESHFRNSMPSPFAVSKEVFLFPT 200
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 107 QYIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTATPILFAVQNVQVPLLSVYVQ 163

QY 201 AANTHLLLLKDAQVFGEEGYSSEDAEFYHROKLTKQYTDHCVNMYNVLNGLRGSTY 260
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 164 AANLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDVAVRYNTGLERVWGPDS 223

QY 261 DAWKKNRRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTELTRDFTDPIPSLNTLOEYGP 320
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 224 RDWVRYNQFRRELTTLVLDIVLFPNYDSRRYPVRTVSQLTREIYNPV-----LENFDG 278

QY 321 TF----LSIENSIRKPHLDYLOGIEPHTRLOQYFGKDSFNVMYSGNYVETRISGSKT 376
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 279 SFRGSAQGIERSIRSHPLMDILNSITIIDAHRGY-----YWSGHQIMASVPVGSFSGPE 332

QY 377 ITSPFYGDK-STEPVOKLSFD-GQKYVRTIANTDVAAPNGKYLGVTKVDFEQYDDQKN 434
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 333 FTFLYGTWGNAAPOQRIVAQLQGQYVRLSST----FYRPPNIGINNQQLSVLDTGTEF 388

QY 435 ETSTQT-----YDSKRNNGHVSAQDSIDQLPETTDEPLEKAYSHQLNYAECLMQDRR 488
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 389 AYGTSNLPASVY---RKSGTV---DSLDEIPPNNNVPPRQGFSHRLSHVSMF----RS 438

QY 489 GT-----IPFTWTHRSVDFENTIDAEKITOLPVKAYALSSGASIEGPGFTGGNL 540
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 439 GSSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVIGSGFTGGDL 497

QY 541 LFLKESNSIAK---FKVTLNSAALLQRYVRIRYASTTNLRFVQNSNDFLVIYINKT 597
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 498 VRLNSSGNIIQNGRYIEVPIHFSTSTRVRYRYASVTPHILNVWNGSSIFSNTVPAT 557

QY 598 MNKDDDLTYQTFDLATNNGMFGSKNELIIGAESFVSNEKIYIDKIEFIPV 650
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 558 ATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNFSGTAGVIIDRFEFIPV 607
```

RESULT 31

USSXSH

parasporal crystal protein cryIaC1 [validated] - Bacillus thuringiensis subsp. kurstaki
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Date: 18-Apr-1984 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A23962; A03489
R;Adang, M.J.; Scaver, M.J.; Rocheleau, T.A.; Leighton, J.; Barker, R.F.; Thompson, D.V.
Gene 36, 289-300, 1985
A;Title: Characterized full-length and truncated plasmid clones of the crystal protein d

A;Reference number: A91526; MUID:86083171; PMID:3000881

A;Accession: A23962

A;Molecule type: DNA

A;Residues: 1-1178 <ADA>

A;Cross-references: UNIPROT:P05069; GB:M11068; NID:g142721; PIDN:AAA22331.1; PID:g142722

A;Experimental source: strain HD-73

A;Note: the authors translated the codon ATT for residue 11 as Leu

R;Wong, H.C.; Schnepf, H.E.; Whiteley, H.R.

J. Biol. Chem. 258, 1960-1967, 1983

A;Title: Transcriptional and translational start sites for the Bacillus thuringiensis cr

A;Reference number: A92410; MUID:93109004; PMID:6296116

A;Accession: A03489

A;Molecule type: DNA

A;Residues: 1-76, 'P', 78-147, 'L', 149-247, 'S', 249-282, 'M', 284-285, 'R', 287-288, 'QN', 291-292

A;Experimental source: strain HD-1

C;Comment: This protein is present in crystalline form as a component of the spore coat.

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 25.5%; Score 867; DB 1; Length 1178;

Best Local Similarity 33.4%; Pred.No.2.3e-47;

Matches 219; Conservative 112; Mismatches 240; Indels 84; Gaps 24;

```
QY 31 DNPNSTLEELNYKEFLRMTESSTEVLNDNSTVDAVGTGISVVG-----QILGWVGVPF 84
   :||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 3 NNPEN-ECIPY----NCLSNPEVEVLGGERIE----TGYTPIDISLSLTQFLSEFVPG 53
```

```
QY 85 AGALTSYQSFNTIWM-----PSDADPWKAPMAQVEVLIDKKIEYAKSKALAEQLQGN 140
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 54 AG----FVLGLVDIIMGIFGPSQ---WDAFLVQIEQLINQRIEFARNAQISRLEGLSNL 106
```

```
QY 141 FEDYVNALNSWKKTPLSLRSKRQDRIRLEFSQAESHFRNSMPSPFAVSKEVFLFPT 200
   || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 107 QYIYAESFREWEADPTN-PALREEMRIQ--FNDMNSALTATPILFAVQNVQVPLLSVYVQ 163
```

```
QY 201 AANTHLLLLKDAQVFGEEGYSSEDAEFYHROKLTKQYTDHCVNMYNVLNGLRGSTY 260
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 164 AANLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDVAVRYNTGLERVWGPDS 223
```

```
QY 261 DAWKKNRRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTELTRDFTDPIPSLNTLOEYGP 320
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 224 RDWVRYNQFRRELTTLVLDIVLFPNYDSRRYPVRTVSQLTREIYNPV-----LENFDG 278
```

```
QY 321 TF----LSIENSIRKPHLDYLOGIEPHTRLOQYFGKDSFNVMYSGNYVETRISGSKT 376
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 279 SFRGSAQGIERSIRSHPLMDILNSITIIDAHRGY-----YWSGHQIMASVPVGSFSGPE 332
```

```
QY 377 ITSPFYGDK-STEPVOKLSFD-GQKYVRTIANTDVAAPNGKYLGVTKVDFEQYDDQKN 429
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 333 FTFLYGTWGNAAPOQRIVAQLQGQYVRLSST----FYRPPNIGINNQQLSVL 383
```

```
QY 430 DDOKNETSTQT-----YDSKRNNGHVSAQDSIDQLPETTDEPLEKAYSHQLNYAECL 483
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 384 DGTEFAYGTSNLPASVY---RKSGTV---DSLDEIPPNNNVPPRQGFSHRLSHVSMER 437
```

```
QY 484 MQDRRCRTI-----PPTWTHRSVDFENTIDAEKITOLPVKAYALSSGASIEGPGFTGG 538
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 438 SGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVIGSGFTGG 496
```

```
QY 539 NLLFLKESNSIAK---FKVTLNSAALLQRYVRIRYASTTNLRLRVQNSNDFLVIYIN 595
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 497 DLVRLNSSGNIIQNGRYIEVPIHFSTSTRVRYRYASVTPHILNVWNGSSIFSNTVP 556
```

```
QY 596 KTWKDDDLTYQTFDLATNNGMFGSKNELIIGAESFVSNEKIYIDKIEFIPV 650
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 557 ATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNFSGTAGVIIDRFEFIPV 608
```

RESULT 32

S32645

parasporal crystal protein cryIaG1 - Bacillus thuringiensis

C;Species: Bacillus thuringiensis

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

[illegible]

Db 374 VVEGVR---FLIARDNNLDSLFLY---RKSGTL---DSFTLPPDESTPPYIGYSHRL 424
Qy 477 NYAE-----CFLMQDRRGITPFFTWTHRSVDFNTIDAEEKITQLPVPVKAYALSSGASIIIE 531
Db 425 CHARFARSPVLEPNFARLPVFWTHRSASPTNEVSPSRITQIPWKAKHTLASSASVIK 484
Qy 532 GPGFTGGNLLFLKE--SSNSIAKFKVTLNSAALLQRYRVRIRYASTNLRFLVQNSNDFL 590
Db 485 GPGFTGGDITMNNINLGDGLRTVTV--TGRLPQSYIRLRVASVANSNGVFRHLPOPSY 543
Qy 591 VVIYNKWKDDLLTYQTFDLATTNSMGFSDKNELIIGAESFVSNKIYIDKIEFIPV 650
Db 544 GISFPRTWGTDEPLTSRSFALTILTPITLTRAQEEF-----NLTIPEGVIIDRIEFVVPV 598
RESULT 41
B42459
hypothetical protein 2 (cryIF 3' region) - Bacillus thuringiensis (strain aizawai) (frag
C:Species: Bacillus thuringiensis
C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: B42459
R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-3976, 1991
A:Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
A:Reference number: A42459; MUID:91286178; PMID:2061280
A:Accession: B42459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <CHA>
A:Cross-references: UNIPROT:Q8KY61; UNIPROT:Q45740; GB:M63897
C:Superfamily: parasporal crystal protein
Query Match 20.6%; Score 700; DB 2; Length 380;
Best Local Similarity 36.6%; Pred. No. 2.2e-37;
Matches 145; Conservative 87; Mismatches 128; Indels 36; Gaps 8;
Qy 1 MNPNNSEHDTI-----KVTNSELQTNHNOYPLADNPSTLEELNYKEFLRMTEDSS 53
Db 1 MKLNPKDKHQSFSSNAKVDKISTDS-----LKNETDIELQINHEDCIKISEYEN 50
Qy 54 TE-VLDNSTVKDAVGIGISVVGQILGVVGFAGALTSPYQSFPLNTIPSDADPKAFMA 112
Db 51 VEPFVSASTIQ-----TGISAGKILGLTGVFPAGQVASLYSFLGELWPKGNQWEIFME 106
Qy 113 QVEVLIDKKTIEYAKSKALAELOGLQNNFEDYVNALNSWKTPLSLRKSQDRIRLEFS 172
Db 107 HVEEIIHQISTVARNKALTDLKGLGDALAVHESLESVWG---NRKNTRRSVKVSQYI 163
Qy 173 QAESHFNSPMSFAVSKFEVLFLPTVQAQANTHLLLLKDAQVGEWGSSEDVAEFYHR 232
Db 164 ALELMFVQKLPSFAVSGEEVPLPIPIYQAANLHLLLRDASIFGKEWGLSSSEISTFYNR 223
Qy 233 QLKLTQOQYTDHCVNWNVYVGLRGSTYDAWVKFNRFRREMTLTVDLIVLPFPYDIRLY 292
Db 224 QVERAGDYSDHCWKVYGTGLNLRGTVAESWVRYNQPRKDMTLMVLDLVALFPSYDTLVY 283
Qy 293 SKGVKTELRDIFTPDIPFSLNTLQY-----GTFLSIENS-IRKDHLPDYLOGIE 342
Db 284 PIKTSQLTREVTYDAIGTHPNPASFASTTWNNAFSTSTIESAVVRNPHLLDFLEQVT 343
Qy 343 FHTRLQPCYFGKGSFNYSNGVNYETRPSIGSSKIT 378
Db 344 IYSLLS-RWSNTQYNNMWGHRLEFRITGGMLNTST 378

RESULT 42
S19306
parasporal crystal protein cry9Aa1 - Bacillus thuringiensis
A:Alternate names: delta-endotoxin, insecticidal crystal protein, parasporal crystal pro
C:Species: Bacillus thuringiensis
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S19306; S23588; A44847; S14837
R:Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrd

FEBS Lett. 293, 25-28, 1991
A:Title: Nucleotide sequence of a novel delta-endotoxin gene cryIg of Bacillus thuringier
A:Reference number: S19306; MUID:92070568; PMID:1660003
A:Accession: S19306
A:Molecule type: DNA
A:Residues: 1-1156 <SMU>
A:Cross-references: UNIPROT:Q99031; EMBL:X58120; NID:g870929; PIDN:CAA41122.1; PID:g40271
A:Experimental source: subsp. galleriae
A:Accession: S23588
A:Molecule type: protein
A:Residues: 24-34 <SMU1>
A:Experimental source: subsp. galleriae
R:Gleave, A.P.; Hedges, R.J.; Broadwell, A.H.
J. Gen. Microbiol. 138, 55-62, 1992
A:Title: Identification of an insecticidal crystal protein from Bacillus thuringiensis Dε
A:Reference number: A44847; MUID:92211329; PMID:1566556
A:Accession: A44847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1151 <GLE>
A:Cross-references: EMBL:X58534; NID:g48879; PIDN:CAA41425.1; PID:g48880
A:Experimental source: isolate DSIR517
A:Note: sequence extracted from NCBI backbone (NCBIN:92865, NCBI:P:92867)
C:Genetics:
A:Gene: cryIG
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 19.9%; Score 679; DB 2; Length 1156;
Best Local Similarity 28.9%; Pred. No. 2.4e-35;
Matches 197; Conservative 129; Mismatches 292; Indels 64; Gaps 21;

Qy 5 NRSEHDTIKVTNPSELQTNHNOYPLADNPSTLEELNYKEFLRMTEDSSTEVLN-NSTVK 63
Db 2 NQNHGILGASGCCASDDVAKYPLANNP-----YSSALNLSQNSILNWINIIG 53
Qy 64 DAVGTGISVVGQILGVVGVFPAGALTSPYQSFPLNTIPSDADPKAFMAQVEVL--IDKK 121
Db 54 DAAKEAVSIGTIVLSLITAPSLTGLISIVYDLIGKVLGSGSQSISDLSCDLSLIDLR 113
Qy 122 IEEYAKSKALAELOGLQNNFEDYVNALNSWKTPLSLRKSQDRIRLEFSQAESHF--- 178
Db 114 VSQVLDNGIADFNGSVLLYLYNLEALDSWNKNP-----NSASAEELTRFRIADSEFDRI 169
Qy 179 --RNSMP---SFAVSKEFEVLFLPTVQAQANTHLLLLKDAQVGEWGS--YSEDVAEFYHR 232
Db 170 LTRGSLTNGGSLARQNAQIALLPSFASAFPHELLLRDATTRYTNWGLYNATPFYINYSK 229
Qy 233 QLKLTQOQYTDHCVNWNVYVGLNGL--RGSTYDAWVKFNRFRREMTLTVDLIVLPFPYDIR 290
Db 230 LVELIELYTDYCVHWNKRGFNLQRGTSATAWLEFHRYREMTLMVLDIVASFSLDIT 289
Qy 291 LYSKGVKTELRDIFTPDIPFSLNTLQYGPFTLS-----IENSIRKPHLEFDYLOGI 341
Db 290 NYPIETDFQLSRVITYDDIFGVHRSLLGESWFSVNRANFSDLENAIPNRPSPFLNNM 349
Qy 342 EPHT--RLQPGYFGKGSFNYSNGVNYETRPSIGSSKITTSPPYGDKSPEPVQKLSFDQK 399
Db 350 IISTGSLTLFVSPSTDRARVWYGS--RDRISPANSQFTELISGQHTTATQTL---GRN 404
Qy 400 VYRTANTDVAWPNKGVYLVGTVDFSQYDDQKNETSTQTYVDSK--RNGG--HVSQAQDSI 456
Db 405 IFR----VDSQACNLNDTTYGVNRAVF--YHDASGSGORSVVEGVIRTTGIDNPRVQIN 458
Qy 457 DOLPPETTDPELEKAYSHQNYAECF-----LMQDRRGITPFFFTWTHRSVDFNTIDAIE 510
Db 459 TYLPGENSDIPTPEDYTHILSTTINLTGLRQVAGNRRSSSLVMYGWTHKSLARNNTINPD 518
Qy 511 KITQLPVWKAYALSSGASIIIEPGTGTGNNLLFLKESNSIAKFKVTLNSAALLQRYRVR 570
Db 519 RITQIPLTKVDRGTGTGVSYNDPFGIGGALL--QRTDHGSLGVLRVQF--PLHURQQRIRKV 576
Qy 571 RYASTTNLRLFVQNSNNDPLVIYIN--KTMNKDDDLTYQTFDLATTNSNMFGSGDKNELI 628

Db 587 PSTTSRQPNATDLTYADFGVYTPRTVPNKTFCGEDTLMLTLYGTPNHSYN--IYDKI 644

Qy 646 EFIPV 650

Db 645 EFIRI 649

RESULT 44

parasporal crystal protein crysAB [validated] - *Bacillus thuringiensis* subsp. *israelensis*.
N:Alternate names: delta-endotoxin Bt8; insecticidal protein ISRH3; mosquitocidal 130K p1
C:Species: *Bacillus thuringiensis* subsp. *israelensis*
C:Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C:Accession: S003398; A37587; JF0315; A28541; I39869; I40584
E:Chungjatupornchai, W.; Hsueh, H.; Seurinck, J.; Angusathanasombat, C.; Vaeck, M.
Eur. J. Biochem. 173, 9-16, 1988
A:Title: Common features of *Bacillus thuringiensis* toxins specific for Diptera and Lepidoptera
A:Reference number: S00398; MUID:88185334; PMID:2833395
A:Accession: S00398
A:Molecule type: DNA
A:Residues: 1-1136 <CHU>
A:Cross-references: EMBL:X07423; NID:Q40353; PDB:1A3A30312 1. PDB:Q40354

Genes 66, 107-120, 1988
Kusumamolo, I.; Wackinson, A.; Kim, L.; Sage, M.V.; Scrutton, R.; Akande, N.; Li, Y.; A:Title: Nucleotide sequence of the gene coding for a 130-kDa mosquitoicidal protein of *B. t. A:Reference number: JT0315: MUID:88129719: PMID:2901387*

A;ACCESSION: A37587
A:Molecule type: DNA

A;Residues: I-50, 'D', 52-64, 'S', 66-192, 'PACI^{TR}RMVY', 202-204, 'C', 207-363, 'LVQIYLKEN', 374, 'YKEELEEPILVONVY', 573-593, 'N', 595-696, 'GIIS', 691-720, 'B', 722-822, 'IIWVSVCN', 823-825, 'WD',

A;Cross-references: GB:M20242; NID:g142737; PIDN:AAA22337.1; PID:g142738
Accession: JN0315

A;Molecule type: protein

A;Note: the majority of sequence differences are consistent with frameshift errors

Nucleic Acids Res. 16, 1637-1638, 1988

A;Reference number: A28541; MUID:88157738; PMID:2831510

A;Molecule type: DNA

A;Cross-references: EMBL:X07082; NID:g40309; PIDN:CAA30114.1; PID:g40310

Agric. Biol. Chem. 52, 873-878, 1988

A;Reference number: I39869

A;Accession: 139803
A;Status: translated from GB/EMBL/DBJ

A; MOLECULE TYPE: DNA
A: Residues: 1-202, 'C'. 205-271, 'L'. 273-324, 'Y'. 326-1136 <RES>

A;CROSS-references: GB:D00247; NID:g216287; PIDN:BAA001/8.1; PID:g216288
R:Angsuthanasombat, C.: Chungiatiapornchai, W.: Kertbundit, S.: Luksanani, P.: Settasatjar

Mol. Gen. Genet. 208, 384-389, 1987

A: Title: Cloning and expression of 130-kd-mosmito-larvicide[delta-endotoxin gene of *Bac*

A;Reference number: I40584; MUID:88038331; PMID:2890080
A;Accession: I40584

A;Status: translated from GB/EMBL/DDBJ

A;Residues: 1-142 <RE2>

C;Comment: This protein is toxic to many lepidopteran larvae.

C;Keywords: delta-endotoxin

Query Match 19.3%; Score 656.5; DB 1; Length 1136;

Matches 188; Conservative 140; Mismatches 260; Indels 77; Gaps 24;

QY 27 YPLADNPSTLEELNYKEFLRMTEDSSSTEVLDNSTV-KDAVGTGISWGIILGWGVPFA 85

Db . 5 YPLANDLOGSMKNTNYKDWLAMCENNOQYGVNPAAINSSSVSTALKVAGAILKFVNPP-A 63


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QY 165 DRIRLFSQAESHERNSPSE-----AVSKFE-----VLFLPTAAQANTHLLLLKDA 212
Db 191 DRVASFDFTANQOHTOHLPEFKNPMWSDENSTOEFKRTSVELTLPMTTIVATLHLLLEYGY 250
QY 213 QVFGEGWGYSSSEDVAEFYHRQLKLTOQYTDHCVN-----WYNVGLNGLRGSTYDAWV 264
Db 251 IEFMTKWNFHNEQ-----YLNLLKVELQOLHSHSVSEVTRTSFLOFLPTLNNRSKSSVNA-- 304
QY 265 KFNRRFRMTLTVLDLIVLPFPVDIRLYSGKVKTELTRIFDTPILSLNLTQYEGTFFLS 324
Db 305 -YNYRYRNNTVNCGLDAATWPTFDTHYHGGGKLDLTRIILSD--TAGPIEBEYTTG--- 357
QY 325 IENSIRKPHLDYLOGIEPHTRLOQCYFGKDSFNYSWGNVETRPS---IGSKKITITSPF 381
Db 358 -----DKTSQPE-HSNITP-----NNILDT-PSPTYQHSFVSDSIV 392
QY 382 YGDKSTPEVQKLSFDGQKVYRTIANTDVAAPNGKVYLGTVKDFSQYDDQNE-----TS 437
Db 393 YSRKELQQLDIATYS-----TNNSNCHPVG---LRLSYTDGSRDYDGNQDPDFTS 441
QY 438 TOTYDSKR-----NNGHV-SAQDSIDL-----PPT 463
Db 442 NNNYCHNSYTABITLVARHLYNAKGLQNVESLVSTVNGSGSGCICDAMINYLPPQT 501
QY 464 T-----DEPLEKAYSHQLNVAECFLMQRRTGTFPFTWTHRSVDFNTI 507
Db 502 SKNESRPDKINVLPIITVTKGTGNGLVISAVPME---LVP-----ENVI 547
QY 508 -DAEKITQLPV--VKAYALSSGASIEGPGFT-----GNNLLFLKSSNSIAKFKVTL 557
Db 548 GQVNAADTKLPLQLKGFPPEKYGEYNNRGISLVREWINGNNA--VKLSNSQSGVGIQTN 605
QY 558 NSAALLQRYRVRIRVASTTNLRLFVQNSNNDFLVIYINKTKMDDLLTQTFDLATTNSN 617
Db 606 QTK--OKYEIRCRYAS-----KGDNN---VYFNVDLSENPPRNSISFG-STESSV 649
QY 618 MFGSGDKNELI-----IGAESF---VSNE---KIVIDKIEFIP 649
Db 650 VGQGENGVKYLKSTTVEIPAGSFVHVITNQSSDLFLDRIEFVP 695

RESULT 49
C32053
parasporal crystal protein B1 - Bacillus thuringiensis subsp. kurstaki
N:Alternate names: parasporal crystal protein P2
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 09-Jul-2004
C:Accession: C32053; A29913
R:Widner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 965-974, 1989
A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki
A:Reference number: A32053; MUID:89123178; PMID:2914879
A:Accession: C32053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <WID>
A:Cross-references: UNIPROT:P21253
R:Donovan, W.P.; Dankocsik, C.C.; Gilbert, M.P.; Gawron-Burke, M.C.; Groat, R.G.; Carlto
J. Biol. Chem. 263, 561-567, 1988
A:Title: Amino acid sequence and entomocidal activity of the P2 crystal protein. An inse
A:Reference number: A29913; MUID:88087146; PMID:3121615
A:Accession: A29913
A:Molecule type: DNA
A:Residues: 1-587, 'FRY' <DON>
C:Genetics:
A:Gene: cryBI

Query Match 7.2%; Score 245.5; DB 2; Length 633;
Best Local Similarity 21.8%; Pred. No. 5.6e-08;
Matches 146; Conservative 96; Mismatches 258; Indels 171; Gaps 29;

QY 62 VKDAVGTGISV-----VGQILG-----VVGVPFAGALTFSFYQSFLNTIWPSDADPWKAPM 111
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Db 50 VAPVVGTVSSFLKKVGLSIGRIILSELNGIIFPGSGTNLMQDILR----- 95
QY 112 AQVEYLIDKKIBEYAKSALAELOQLNNFEDY-----VNALN-SWKKTPLSLRSKRSQDR 166
Db 96 -ETEQLAQLRLNTDTLARVNAELIQLQANIREFNQOVDFLNPTQNPVPLSITS--SVNT 152
QY 167 IRELSQAESHPRNSPFAVSKFEVLFLPTAAQANTHLLLLKDAQVFGEGWGYSSDEV 226
Db 153 MOOL-----FLNRLPQFQGYQLLLPLFAQANMHLSEFIRDVLNADGWSAAATL 205
QY 227 AEFYHRQLKLTOQYTDHCVNWYNVGLRGSTYDAWVKFNFRREMTLTVLDLVLPPF 286
Db 206 RYRDYRLNRYFDYNYCINITYQTAFRGLNRLHD---MLEFRYMFANVEYVSIWSL 261
QY 287 YDIR-----LVSKGVKTELTRDI-----FTDPIFSLMT---LOEYGTFFLSIENS 328
Db 262 PKYQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYLSLGSIGTRLSI--- 318
QY 329 IRKPHLDYLOGIEPHTRLOQCYFGKDSFNYSWGNVETRPSIGSKKITITSPFYGDKSTE 388
Db 319 -----TFPNIGL-----PGSTTHLSNARSVNY-----SGGVSSGLIGATNLN 357
QY 389 PVQKLSFDGQKVYRTIANTDVAAPNGKVYLGTVKDFSQYDDQNETSTQYDYSKRNNG 448
Db 358 H-----NFNCSTVLPPLSTPFVRSWLDs---GTDREGVATSTNQTE-SFOITLSLR-CG 407
QY 449 HVSQAQSDIDQLPP-----ETTDPL---EKAYSHQLNVAECFLMQRRTG---IPFTWT 497
Db 408 AFSAGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPGTGGARAYLSV 467
QY 498 HRSVDFFNTIDA-----EKITQLPVKAYAL-----SSGASIEGPGFTGGNLL 541
Db 468 HNRK---NNIYAENGTMIHLAPEDYTGFTISPISHATQVNNQTRTFISEKFGNQDSLR 524
QY 542 FLKSSNSIAKFKVYKVLNSAALLQRYRVRIRVASTTNLRLFVQNSNNDFLVIYINKTKMD 601
Db 525 F-EQSNITARTYLRGNG---NSYLVLRVSSIGNSTIRVTINGRVVTVSNVNTTND 578
QY 602 -----DLTYOTFDL-ATTNSNMGFSFGDKNELIIGAESFVSNEKIY 641
Db 579 GVNDNGARFSDINIGNIVASDNTNVTLDINVLNSGTGTFD----- 618

QY 642 IDKIEFIPVQL 652
Db 619 LMNMFVPTNL 629

RESULT 50
D32053
parasporal crystal protein B2 - Bacillus thuringiensis subsp. kurstaki
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 13-Jul-1989 #sequence_revision 13-Jul-1989 #text_change 09-Jul-2004
C:Accession: D32053; S12396
R:Widner, W.R.; Whiteley, H.R.
J. Bacteriol. 171, 965-974, 1989
A:Title: Two highly related insecticidal crystal proteins of Bacillus thuringiensis subsp. kurstaki
A:Reference number: A32053; MUID:89123178; PMID:2914879
A:Accession: D32053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <WID>
A:Cross-references: UNIPROT:P21254
R:Dankocsik, C.; Donovan, W.P.; Jany, C.S.
Mol. Microbiol. 4, 2087-2094, 1990
A:Title: Activation of a cryptic crystal protein gene of Bacillus thuringiensis subsp. kurstaki
A:Reference number: S12396; MUID:91211618; PMID:2089222
A:Accession: S12396
A:Molecule type: DNA
A:Residues: 1-633 <DAN>
A:Cross-references: EMBL:X55416; NID:940311; PIDN:CAA39075.1; PID:940312
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Query Match		7.2%	Score 245;	DB 2;	Length 633;
Best Local Similarity		19.5%	Pred. No. 6.1e-08;		
Matches 128;		Conservative 92;	Mismatches 235;	Indels 200;	Gaps 23;
Qy	83	PFAGALTSF-----	YQSFNTIWP-	DADPWKAFMAQVEVLIDKKIEYAKS	128
Db	52	PIVGTVASFLKKVGSVUGKRILSELNLI	PPSGSTNLMQDILRETEKFLNQRLNTDTLA	111	
Qy	129	KALAEQGLQNNFEDYVNALNSW-----	KKTPLSLRSKRQDRIRLFSQAESHFRNSMP	183	
Db	112	RVNAELTGLQANVEEFNRQVDNPLNPNR	NAVPLSITS--SVNTMQQL-----	FLNRLP	162
Qy	184	SFAVSEFVLFLPTYAAQANTHLLLLKDAQ	VFGEENGYSSEDAEFVHROLKLTQQYTDH	243	
Db	163	QFQMGGYQLLLPLFAQAANLHLSFIRDV	ILNADENGISAATLRTYRDYLNKNTDYDNY	222	
Qy	244	CVMWYVGLNLRGSGTYDAWVKNRFRRENT	TLVLDLVLFPFYDIR-----	LYSK	294
Db	223	CINTYQSAFKGLNRLHD----	MLEFRTYMLNVEFYVSIWSLKYQSLVSSGANLYAS	278	
Qy	295	GVKTELTRDI-----	FTDPIFSLNT-----	LQEYGTFLSIENSIRKPHLF--	335
Db	279	GSGFQQTQSFTSDWPFLYSFLQVNSYV	LVNGFSGARLSNTFFNIVGLPGSTTHALLAA	338	
Qy	336	--DYLOGIEFHTRLQPGYFGKDSFNY--	-----	-----	359
Db	339	RVNYSGGI-----	SSGDIGASPFNQFNCSFTLPLLT	PPFVRSWLDSDSGDREGVATVTN	392
Qy	360	WSGNYVETRESI-----	GSSKITSPFYGDKSTEPVOKLSFDGQKV--	YRTIANTDV	409
Db	393	WQTESFETTLGLRSGAFTARGNSNYFPDY	FIRNISGVPLVVRNEDLRRPLHYNEIRN---	449	
Qy	410	AAWPNG-----	KVVLGVTKVDFSQDDQKNETSTQTYDS	KRNNGHVSQAQDS--IDQLPPE	462
Db	450	IASPSGTGPGARAYM-----	-----	VSVHNRKNNIHAVHENGSMIHLAPND	490
Qy	463	TTDPELEKAYSHQVNAECFLMQDRRG	TIPFTWTHRSVDFFNTIDAEDITQLPVVKAYA	522	
Db	491	YTGFTTSPIHATQVNNQ-----	-----	TRTFISEKFGNGDLSLRFQNNTTARYT	535
Qy	523	LSSGASIIIEGPGTGGNL--	LFLKESNSIAKFKVTLNSAALLQRYVRIRYASTNLR	L 580	
Db	536	LRG-----	NGNSYNLYLRVSSIGNSTIRVING-----	RVYTATNVNT	573
Qy	581	FVON-----	SNNDPLVIVINKTMNKDDDLTYQTFLATTN	615	
Db	574	TTNNDGVNDNGARFSDINIGNVVASNS	VDPLDINVTLNSGTQFDLMNIMLVPTN	628	

Search completed: February 14, 2005, 15:24:14
Job time : 65 secs

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